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cca gag cgc g Pro Glu Arg A 215								787
atc gtc aag of Ile Val Lys (230	Gln Gly I	cct aag Pro Lys 235	ggt gtc Gly Val	atg gcg Met Ala 240	atg acc Met Thr	aag gac Lys Asp	gaa Glu 245	835
acc gta gaa q Thr Val Glu V								883
gcc ggc gat o								931
tgg ccg ttg (Trp Pro Leu (280		Val Leu				Gly Ala		979
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Gln Ser Phe G	Gly Lys 1	Tyr Leu	Gly Gly 40	Ser Ala	Ala Asn 45		Val	
Ala Ala Ala A	Arg His (Gly His 7	Asn Ser	Ala Leu	Leu Ser 60	Arg Val	Gly	
Asn Asp Pro 1 65	Phe Gly (Glu Tyr : 70	Leu Leu	Ala Glu 75	Leu Glu	Arg Leu	Gly 80	
Val Asp Asn (Cln Tur 1	י בומובט	Thr Asn	Gln Thr	Phe Luc	Thr Pro	Val	

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser 115 120 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly 130 135 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr 145 150 155 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met 165 170 175

Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu 180 185 190

Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala 195 200 205

Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg 210 215 220

Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala 225 230 235 240

Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val 245 250 255

Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His 260 265 270

Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn 275 280 285

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Met Thr Asn Leu Thr

age act cae gaa gte eta get ate gge ege ttg gge gta gat att tae 163 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr

10 15 20 cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211 Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys 25 259 tac etc ggc gga agc gca gca aac gtt tet gtt gca gcc gcc egc cat Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His 40 45 gga cac aat tee gea etg etg tee egt gtg gga aat gat eet tte gge 307 Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac 355 Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr 70 gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403 Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile 90 95 100 tto coa cog gat gat tto coa ctg tac tto tac cgc gaa coa aag got 451 Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala 105 110 ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499 Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg 120 125 130 gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547 Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro 135 140 age ege age aca cae ege gag ate ttg act act egt geg aac egt ege Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg cac acc atc ttt gat ctg gac tac cga 622 His Thr Ile Phe Asp Leu Asp Tyr Arg 170 <210> 330 <211> 174 <212> PRT <213> Corynebacterium glutamicum <400> 330 Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly

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Thr Phe Cys Glu		Pro Pro	Asp Asp 105	Phe P	ro Leu	Tyr P 110	he Tyr	
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Leu Asp Asp Val	Arg Glu	Ala Asp 135	Ile Leu	_	he Thr 40	Leu T	hr Gly	
Phe Ser Glu Glu 145	Pro Ser 150	Arg Gly	Thr His	Arg G 155	lu Ile	Leu T	hr Thr 160	
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ctgactacga tggt ctgactacga tggt cct caa atc ggc Pro Gln Ile Gly caa ttc cgc gat Gln Phe Arg Asg 25 tgg cgt cta acc Trp Arg Leu Thr 40 aat gtg gaa gaa Asn Val Glu Glu	tcc cgc Ser Arg 10 ctc gac Leu Asp cca gca Pro Ala aaa gcg Lys Ala	ctc tct Leu Ser ggc gac Gly Asp gag cgt Glu Arg 45 ggc ctg Gly Leu 60 ccg gag	cgt gtc Arg Val 15 ggc gta Gly Val 30 gcc gct Ala Ala atg atc Met Ile	att g Ile G Ctt g Leu A gac c Asp L atc g Ile G	tg tct let Ser 1 laa caa clu Gln lca cct la Pro ltg gtg leu Val 50 gt tcg ly Ser 65 aa gac	caa gGln GG gac gAsp GTyr G35 aaa cLys A	ag cgg lu Arg 5 gc cta ly Leu 20 aa gat lu Asp gt atg rg Met ac ccc yr Pro aa aag	115 163 211 259

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cct cgt aac c Pro Arg Asn H					
gcg ggt gtg t Ala Gly Val P 1					
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gct tct gag c Ala Ser Glu P 230					
ccg gag ttg a Pro Glu Leu I					
Gly Pro Glu I			tcg acc acc a		
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ctg cct cct t Leu Pro Pro P 310					
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gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asp Glu 425 430 435	
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gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Let 470 475 480	
cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro 490 495 500	o Glu
gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser 505 510 515	
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Ala	Pro	Tyr 35	Glu	Asp	Trp	Arg	Leu 40	Thr	Pro	Ala	Glu	Arg 45	Ala	Ala	Asp
Leu	Val 50	Lys	Arg	Met	Asn	Val 55	Glu	Glu	Lys	Ala	Gly 60	Leu	Met	Ile	Ile
Gly 65	Ser	His	Tyr	Pro	Gly 70	Tyr	Ser	Pro	Leu	Ala 75	Pro	Glu	Ser	Glu	Gl y 80
Lys	Asp	Ala	Glu	Lys 85	Cys	Glu	Pro	Leu	Leu 90	Asn	Pro	Val	Asp	Met 95	Trp
Arg	Glu	Asp	Asn 100	Pro	Ile	Thr	Gly	Val 105	Pro	Phe	Thr	Glu	Pro 110	Val	Leu
Ala	Thr	Ser 115	Ser	Thr	Glu	Asn	Ala 120	Ile	Asn	Leu	Arg	Asn 125	Gln	Arg	Туг
Leu	Ile 130	Val	Arg	Asp	Asn	Leu 135	Pro	Ala	Arg	Gly	Leu 140	Ala	Thr	Trp	Thr
Asn 145	Ala	Val	Gln	Glu	Val 150	Ala	Glu	Arg	Ser	Arg 155	Leu	Gly	Ile	Pro	Val 160
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Gly	Val	Asn	Glu 180	Ser	Ala	Gly	Val	Phe 185	Ser	Glu	Trp	Pro	Gly 190	Glu	Lev
Gly	Leu	Ala 195	Ala	Leu	Arg	Asp	Ala 200	Glu	Leu	Met	Glu	Thr 205	Phe	Gly	Thr
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Thr	Phe	Gly	Glu	Asp 245	Pro	Glu	Leu	Ile	Ser 250	Asp	Tyr	Ile	Ala	Ala 255	Val
Val	Arg	Gly	Leu 260	Gln	Gly	Pro	Glu	Leu 265	Ser	Lys	Asn	Ser	Val 270	Ser	Thr
Thr	Ile	Lys 275	His	Phe	Pro	Gly	Gly 280	Gly	Val	Arg	Leu	Asp 285	Gly	His	Asp
Pro	His 290	Phe	His	Trp	Gly	Gln 295	Thr	Asn	Glu	Tyr	Pro 300	Thr	Glu	Asp	Ala
Leu 305		Lys	Tyr	His	Leu 310		Pro	Phe	Gln	Ala		Ile	Asp	Ala	Gly

Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser 425 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu 440 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp 470 Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro 520 Arg Gly Asn Leu Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro 545 <210> 333 <211> 1607 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1584) <223> FRXA00799 cta caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu 10

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											tgg Trp					240
											ctg Leu					288
											tac Tyr					336
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											ttc Phe					480
										-	ctg Leu			_		528
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											gtt Val					720
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Phe	Pro	Gly	Gly 260	Gly	Val	Arg	Leu	Asp 265	Gly	His	Asp	Pro	His 270	Phe	His	
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								aac Asn								960
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_	_					_	_	gcc Ala				_	_	-		1440
_	•							ccg Pro			-	_	_			1488
								cgc Arg								1536

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1607

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Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu
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Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn 65 70 75 80

Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser 85 90 95

Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg 100 105 110

Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln
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Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser 130 135 140

Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu 145 150 155 160

Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala 165 170 175

Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys 180 185 190

Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp 195 200 205

Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu 210 215 220

Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu 225 230 235 240

Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His

245 250 255

Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His 260 265 270

Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr 275 280 285

His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile 290 295 300

Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp 305 310 315 320

Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe 325 330 335

Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly 340 345 350

His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met 355 360 365

Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Val 370 375 380

Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu 385 390 395 400

Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asp Gln 405 410 415

Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu 420 425 430

Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro 435 440 445

Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu 450 455 460

Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro 465 470 475 480

Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser 485 490 495

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			ttc Phe													787
			gtg Val													835
			gac Asp													883
			cca Pro 265													931
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			gaa Glu 425													1411
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	c tcc ttc aaa cac ggc gac n Ser Phe Lys His Gly Asp 60	
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	g ctc att gtt cgc agt gaa g Leu Ile Val Arg Ser Glu 125	
	a ccc cgc gga tct tta tcc o Pro Arg Gly Ser Leu Ser 140	
His His Gln Arg Cys	c ttt gat ccc gta tca cac s Phe Asp Pro Val Ser His 155 160	Arg Pro Asp Arg Arg
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acc cgc gag Thr Arg Glu 295											1027
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Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln 50 55 60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser 65 70 75 80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
85 90 95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg 100 105 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met 115 120 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro 130 135 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp 145 150 155 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr 165 170 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe 180 185 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala 195 200 205

Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe 210 215 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe 280 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly 300 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn 330 325 His Ala Ile Tyr Gln Glu Leu Leu Pro Glu Gly Glu Ser Gly Val 345 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly 355 360 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln <210> 349 <211> 720 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(720) <223> RXA02026 <400> 349 cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp

gac tta ata Asp Leu Ile 50			Glu Gly							192
aaa tat gad Lys Tyr Asi 65										240
ggg cat tta Gly His Le		Met Tyr								288
caa cga cat Gln Arg His				Arg						336
gtt gaa aaq Val Glu Ly: 11	Phe Pro					Gln P				384
aca agt cat Thr Ser His 130	-	-	Lys Val		Lys T	_				432
tat gca ato Tyr Ala Ilo 145				Asp						480
ctt tat aas Leu Tyr Ass	_	Asp Ile						_		528
aat aca gad Asn Thr Glu	-	-		Met		-	-	-		576
ttt aat tta Phe Asn Lem 19	ı Asp Asn					Cys P				624
gaa cca aaa Glu Pro Lys 210			Lys Asr		Tyr (Gln S				672
ctt gga aad Leu Gly Ly: 225				Thr						720
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PCT/IB00/00943 WO 01/00844

Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr 120 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr 135 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gly Arg Leu Leu 155 145 150 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr 180 185 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe 230 235

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ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg

115

Gly	Tyr	His	Arg	Pro 10	Glu	Leu	His	Ile	Thr 15	Ala	Glu	Ser	Gly	Val 20	Leu	
ttt Phe	gca Ala	cct Pro	gca Ala 25	ggc Gly	gtt Val	ctg Leu	ttg Leu	gat Asp 30	gac Asp	gac Asp	acg Thr	tgg Trp	cat His 35	ttc Phe	ttc Phe	211
									ggc Gly							259
									gat Asp							307
									cgc Arg							355
									acc Thr 95							403
									aac Asn			Gly				451
ctg Leu	atc Ile	aat Asn 120	gag Glu	gac Asp	gag Glu	ctg Leu	ggg Gly 125	ctc Leu	gat Asp	cca Pro	gat Asp	gtc Val 130	tcc Ser	cga Arg	atc Ile	499
									tat Tyr							547
									gga Gly							595
									ggc Gly 175							643
									aga Arg							691
		Ser							tta Leu							739
		200					203									
		cct					ctg		gat Asp			gat				787
Val	Ala 215 gat	cct Pro	Arg	Met	Ile gtc	Arg 220 acc	ctg Leu	Arg		Glu gac	Val 225 ggg	gat Asp att	His gac	Glu att	Ile tcg	787 835

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	Ile Asp Phe		ttc tct cgc ccc Phe Ser Arg Pro 275	
acc aac tac gcc Thr Asn Tyr Ala 280	gaa acc acc Glu Thr Thr	atc ggc tac Ile Gly Tyr 285	c gac ttc gcc cac c Asp Phe Ala His 290	atc ttt 979 Ile Phe
			c tee eee act gag o Ser Pro Thr Glu 305	
agt tgg aag gaa Ser Trp Lys Glu 310	gaa ggc tgg Glu Gly Trp 315	gca aac gct Ala Asn Ala	att tot tto coa Ile Ser Phe Pro 320	cgt att 1075 Arg Ile 325
			g acc cct cca gaa n Thr Pro Pro Glu 5	
	His Glu Ser		g gca ggt tgg acc a Ala Gly Trp Thr 355	Gly Leu
			a gtg gcg ttg aag 1 Val Ala Leu Lys 370	
			c cgc cac aat cag s Arg His Asn Gln 385	
			g ggt gat cca cac a Gly Asp Pro His 400	
			a ctg ttc att gtc r Leu Phe Ile Val 5	
	. Glu Val Phe		c ggt tat gta toa y Gly Tyr Val Ser 435	Met Ala
agc cgt gtg tat Ser Arg Val Tyr 440	ttc aac aac Phe Asn Asn	gga cca tto Gly Pro Phe 445	c agc gaa ttt gag e Ser Glu Phe Glu 450	gtc acc 1459 Val Thr
			g gaa agt cac tto n Glu Ser His Phe 465	
			gat ctc act gcg Asp Leu Thr Ala 480	
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Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile 50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro 165 170 175

Val Glu Ala Pro Thr Val Val Leu Asp Ser Pro Asp Gly Arg Glu 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp 225 230 235 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu 245 250 255

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe 260 265 270

Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp 280 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val 360 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg 375 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly 385 390 395 Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly 420 425 Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser 440 Glu Phe Glu Val Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro 490 495

Val Arg

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1 ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163 Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp 10 ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211 Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc 259 Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu 45 307 aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val 55 gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca 355 Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala 70 gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala 90 95 100 cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca 451 Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala 105 110 ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val 120 125 get etc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac 547 Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn 135 acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595 Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr 150 ege age atg ete ace qte qae aac qag gaa gaa tee ete ege gea etg Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu 170 ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691 Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile 185 gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739 Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg 200 205 gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787 Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu 215 220 cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc 835 Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe

230

tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu 250 255 260	883
cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp 265 270 275	931
aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu 280 285 290	979
ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp 295 300 305	1027
gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu 310 315 320 325	1075
ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His 330 335 340	1123
gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu 345 350 355	1171
gca ggg gag aag acc ctc gaa gta gca ggt cac gcc gca tgg gtt Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val 360 365 370	1219
cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val 375 380 385	1267
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Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile 35 40 45	
Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala 50 55 60	
33 00	

65					70					75					80
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Ser	Leu	Glu	Gln 100	Ala	Arg	Glu	Gly	Phe 105	Ala	Arg	Glu	Asn	Ser 110	Ala	Gly
Ile	Asp	Leu 115	Gly	Ala	Pro	Asn	Arg 120	Asn	Tyr	Arg	Asp	Pro 125	Asn	His	Lys
Pro	Glu 130	Leu	Ile	Val	Ala	Leu 135	Thr	Glu	Phe	Ile	Ala 140	Met	Ala	Gly	Phe
Arg 145	Pro	Leu	Arg	Asn	Thr 150	Leu	Thr	Ile	Phe	Asp 155	Ala	Leu	Ala	Cys	Glu 160
Pro	Leu	Asp	Arg	Туг 165	Arg	Ser	Met	Leu	Thr 170	Val	Asp	Asn	Glu	Glu 175	Glu
Ser	Leu	Arg	Ala 180	Leu	Phe	Thr	Thr	Trp 185	Ile	Thr	Ile	Pro	Ile 190	Gly	Lys
Arg	His	Glu 195	Leu	Ile	Asp	Ala	Leu 200	Ile	Ser	Asn	Ala	His 205	Thr	Tyr	Leu
Glu	Ala 210	Ser	Asp	Arg	Asp	Glu 215	Asp	Ile	Ala	Phe	Val 220	Leu	Ser	His	Ile
Ile 225	Glu	Leu	Asn	Glu	Gln 230	Tyr	Pro	Gly	Asp	Val 235	Gly	Val	Leu	Gly	Ala 240
Leu	Leu	Leu	Asn	Phe 245	Tyr	Lys	Leu	Ala	Pro 250	Gly	Glu	Ala	Leu	Tyr 255	Leu
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Met	Ala	Asn 275	Ser	Asp	Asn	Val	Leu 280	Arg	Gly	Gly	Leu	Thr 285	Ser	Lys	Tyr
Val	Asp 290	Val	Pro	Glu	Leu	Val 295	Arg	Val	Leu	Asp	Phe 300	Asn	Ser	Leu	Glu
Asn 305	Ala	Arg	Val	Asp	Val 310	Glu	Glu	Asp	Gly	Ala 315	Thr	Thr	His	Tyr	Pro 320
Val	Pro	Ile	Asn	Glu 325	Phe	Gln	Leu	Asp	Arg 330	Val	Ala	Val	Gln	Gly 335	Glu
Ala	Glu	Ala	Asn 340	His	Asp	Gly	Pro	Met 345	Ile	Val	Leu	Cys	Thr 350	Ser	Gly
Thr	Val	Ser 355	Leu	Glu	Ala	Gly	Glu 360	Lys	Thr	Leu	Glu	Val 365	Ala	Ala	Gly
His	Ala 370	Ala	Trp	Val	Pro	Ala 375	Asn	Asp	Pro	Thr	Ile 380	Ala	Met	Arg	Ser
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aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca
                                                                   96
Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
aac ett eac gea tae ate age gge ete gge gta gag ate atg geg aac
                                                                   144
Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
                             40
tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc
                                                                   192
Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc
                                                                   240
Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
gtg gac gtt gaa gac ggt gca acg acc cac tac cca gtt cca atc
                                                                   288
Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc
                                                                   336
Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
                                105
aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc
                                                                   384
Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
                            120
                                                                   432
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Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
                        135
tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca
                                                                   480
Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
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<212> PRT

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Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn 35 40 45

Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val 50 60

Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg 65 70 75 80

Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile 85 90 95

Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
100 105 110

Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser 115 120 125

Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala 130 135 140

Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala 145 150 155 160

Glu Val Phe Leu Ala Arg Val 165

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Met Glu Leu Leu Glu
1 5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163 Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp 10 15 20

ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211 Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp 25 30 35

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	gaa Glu 55															307
	gaa Glu															355
	gga Gly															403
_	gaa Glu			-	-				-			_			_	451
_	aac Asn	-			_	-				_			_		_	499
	ctc Leu 135															547
	ctc Leu															595
	agc Ser															643
	acc Thr															691
-	gcc Ala			Ser	Asn	-	His	Thr	Tyr	Leu	Glu	-	Ser	-	-	739
	gag Glu 215															787
	tac Tyr															808
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<400> 358

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Lys	Ile	Glu	Ala 20	Gly	Gln	Gly	Ser	Asp 25	Glu	Leu	Tyr	Asn	Asp 30	Phe	Glu	
		-	cag Gln	_			-	-				_				144
-			gcg Ala			_	-	_			_		_			192
-	-	-	gca Ala	-		_						_	-			240
		-	ctt Leu		-	_	-	-	_	-	•	-		-		288
· ctg Leu			cgt Arg 100													336
			cct Pro													384
_			act Thr		_			-	_		_		_	-		432
_	-		ttc Phe	-		-			_	_			_			480
			cgc Arg													528
			tcg Ser 180													576
			ccg Pro													624
-	_	-	cgg Arg	-			_	-	-	_		-		_	_	672
_	_	-	cct Pro	-					-	_		_				720
			gct Ala													768
_		-	gat Asp							_		-	-	_	_	816

260 265 270

atc t Ile T	ac Tyr	gaa Glu 275	gag Glu	gtc Val	tat Tyr	cgt Arg	gtg Val 280	gtg Val	aag Lys	ttc Phe	tgg Trp	gtg Val 285	gat Asp	ttg Leu	ggt Gly	864
gtg a Val T 2																912
tgg c Trp G 305																960
ttc c Phe L																1008
aag a Lys I																1056
aac g Asn G							-				_		_		_	1104
att t Ile S		-	-		_						_		_			1152
tct c Ser L 385																1200
gcc g Ala A																1248
ttt g Phe G																1296
gag a Glu I																1344
ggc g Gly A																1392
gcg a Ala A 465																1440
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aat a Asn T																1536

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His	Gly	Ala 35	Gln	Leu	Phe	Glu	Arg 40	Ala	Ala	Glu	Asn	Leu 45	Ser	Lys	Glu	
Asp	Arg 50	Thr	Ala	Leu	Phe	Asp 55	Val	Ala	Ser	Ser	Leu 60	Arg	Arg	Gly	Gly	
Asp 65	Val	Arg	Ala	Arg	Leu 70	Ala	Pro	Ala	Leu	Thr 75	Ala	Ser	Val	Thr	His 80	
Leu	Leu	Glu	Leu	Asn 85	Pro	Leu	Arg	Glu	Leu 90	Val	Thr	Met	Gly	Glu 95	Asn	
Leu	Gln	Val	Arg 100	Val	Glu	Arg	Arg	Ala 105	Ala	Leu	Val	Asn	Ser 110	Trp	Tyr	
Glu	Leu	Phe 115	Pro	Arg	Ser	Thr	Gly 120	Gly	Trp	Asp	Glu	Ser 125	Gly	Thr	Pro	
Val	His 130	Gly	Thr	Phe	Ala	Thr 135	Thr	Ala	Gln	Ala	Leu 140	Glu	Arg	Val	Ala	
Lys 145	Met	Gly	Phe	Asp	Thr 150	Val	Tyr	Phe	Pro	Pro 155	Ile	His	Pro	Ile	Gly 160	
Glu	Val	Asn	Arg	Lys 165	Gly	Arg	Asn	Asn	Thr 170	Leu	Thr	Pro	Glu	Pro 175	His	

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp 185 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu 215 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly 280 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe 295 300 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile 315 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser 330 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr 345 340 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp 360 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala 375 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg 440 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala 475 Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu

505

500

510

Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala 520 Gln Phe Glu Val Arq Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser 535 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp 570 Arg Glu Ile Lys Thr Tyr Arg Ala 580 <210> 361 <211> 2316 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2293) <223> RXA02612 <400> 361 gaacttccag cgtctcgccg tgagcgtctc gcgtggcgcg aaatcaagac ctaccgcgcg 60 taatttccca tctctgtacc ttctatcaag gattatcatc atg acc gtt gac ccc 115 Met Thr Val Asp Pro gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac 163 Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa 211 Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu 259 get ggt teg gtt ate ege aeg ege eag gte gge geg aeg eag gtt aat Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn 307 ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355 Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu 403 gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr 95 tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag 451 Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu

105 110 115

					ttg Leu											499
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					ggc Gly 155											595
					ccg Pro											643
	_				ggc Gly			-		•					-	691
					ggc Gly											739
cgt Arg	cgc Arg 215	gca Ala	gaa Glu	ctg Leu	gcg Ala	ccg Pro 220	gca Ala	acc Thr	gga Gly	tct Ser	att Ile 225	gtc Val	gct Ala	tcc Ser	tct Ser	787
gag Glu 230	tac Tyr	cag Gln	tgg Trp	cag Gln	gat Asp 235	tcc Ser	gag Glu	tgg Trp	ctg Leu	cgc Arg 240	gag Glu	cgt Arg	tcc Ser	caa Gln	act Thr 245	835
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					cgc Arg											1123
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ggc acc Gly Thr 375			Asp											1267
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cgc gtc Arg Val	gac go Asp A	cc gtg la Val 410	gcc (tcc Ser	atg Met	ctg Leu	tac Tyr 415	ctc Leu	gat Asp	tac Tyr	tcc Ser	cgt Arg 420	gag Glu	1363
cac ggc His Gly	Glu T													1411
gca gtg Ala Val	cag to Gln Pi 440	tc ctg he Leu	cag (Gln (gaa Glu	atg Met 445	aac Asn	gcc Ala	acg Thr	gtg Val	ctg Leu 450	cga Arg	ctg Leu	cac His	1459
cct ggt Pro Gly 455			Ile i											1507
acc gca Thr Ala 470														1555
atg ggc Met Gly														1603
cac cgc His Arg	Ala P													1651
ttc tct Phe Ser														1699
ggc aag Gly Lys 535			Trp /											1747
gcc gct Ala Ala 550														1795
aag aag Lys Lys														1843
gct gaa Ala Glu	Gly G		_			-		_	-					1891

						cgc Arg										1939
						ctg Leu 620										1987
				-		gac Asp	-	_					_			2035
	-			_	-	ggc Gly		-	_	-	-	-			-	2083
				-		gag Glu		-			-	-				2131
						aac Asn										2179 .
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met 1	1111	Val	Asp	5	HIG	Ser	птз	116	10	116	PIO	GIU	HIG	15	Leu	
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Pro 65	Ile	Gly	Asp	Asp	Ile 70	Phe	Ala	Ile	Asp	Leu 75	Gly	His	Arg	Glu	Arg 80	
Ala	Asp	Tyr	Arg	Leu 85	Glu	Val	Thr	Trp	Pro 90	Asp	Gln	Glu	Pro	Gln 95	Val	

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Val	Leu 450	Arg	Leu	His	Pro	Gly 455	Ala	Leu	Thr	Ile	Ala 460	Glu	Glu	Ser	Thr
Ser 465	Trp	Pro	Gly	Val	Thr 470	Ala	Pro	Thr	Trp	Asp 475	Gly	Gly	Leu	Gly	Phe 480
Ser	Leu	Lys	Trp	Asn 485	Met	Gly	Trp	Met	His 490	Asp	Thr	Leu	Glu	Tyr 495	Phe
Ser	Lys	Asn	Pro 500	Val	His	Arg	Ala	Phe 505	His	His	Ser	Glu	Leu 510	Thr	Phe
Ser	Leu	Val 515	Tyr	Ala	Phe	Ser	Glu 520	Arg	Phe	Val	Leu	Pro 525	Ile	Ser	His
Asp	Glu 530	Val	Val	His	Gly	Lys 535	Gly	Ser	Leu	Trp	Asp 540	Arg	Met	Pro	Gly
Asp 545	Thr	Trp	Asn	Lys	Ala 550	Ala	Gly	Leu	Arg	Thr 555	Phe	Leu	Ala	Tyr	Met 560
Trp	Ser	His	Pro	Gly 565	Lys	Lys	Leu	Leu	Phe 570	Met	Gly	Gln	Glu	Phe 575	Gly
Gln	Arg	Glu	Glu 580	Trp	Ala	Glu	Gly	Gln 585	Gly	Leu	Pro	Trp	Asp 590		Val
Asp	Gly	Trp 595	Gln	Gly	Glu	Tyr	His 600	Glu	Ala	Ile	Arg	Thr 605	Leu	Thr	Arg
Ser	Leu 610	Asn	Gly	Val	Tyr	Ser 615	Asp	Ser	Pro	Ala	Leu 620	His	Thr	Gln	Asp
Phe 625	Thr	Gly	Glu	Gly	Phe 630	Thr	Trp	Asn	Lys	Gly 635	Asp	Asp	Ala	Thr	Asn 640
Asn	Ile	Leu	Ala	Phe 645		Arg	Phe	Gly	Ser 650		Gly	Ser	Gln	Met 655	Leu
Cys	Val	Phe	Asn 660	Leu	Ser	Gly	Thr	Ser 665	Gln	Pro	Glu	Tyr	Gln 670	Leu	Gly
Val	Ala	Ala 675	Gly	Gly	Glu	Trp	Lys 680	Leu	Val	Leu	Asn	Thr 685	Asp	Asp	Ala
Glu	Phe 690	Leu	Gly	Ala	Glu	Asn 695	Asp	Ile	Ala	Thr	Ser 700	Val	Gln	Ala	Ala
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tac cgc gad Tyr Arg Asp 210	-	-				_	_	672
ggt gaa tto Gly Glu Phe 225	Ala Ser							720
aac ggc cgt Asn Gly Arg	-	-	er Ile			_	-	768
ggc ttc acc Gly Phe Thi								816
gcc aac ggt Ala Asn Gly 275	Glu Asp	Gly Arg A		_		_		864
aac tgt ggo Asn Cys Gly 290								912
cgt gct cag Arg Ala Glr 305	Gln Arg							960
ggc acc cct Gly Thr Pro		_	ly Asp	-	-			1008
ggc aac aac Gly Asn Asi	-	_	-	_				1056
tgg gat cag Trp Asp Glr 355	Ala Glu	Glu Asn A						1104
ttg ctg cgt Leu Leu Arc 370	-	-		Val Phe				1152
ctt gcc ggt Leu Ala Gly 385	Gly Pro							1200
tgg ctg gta Trp Leu Val			eu Met					1248
gct ttc ggt Ala Phe Gly								1296
gag cct gat Glu Pro Asp 435	Tyr Arg	Gly Gln L		_	_		_	1344

atg ttc aac Met Phe Asn 450			Pro Il								1392
cat ttc ggt His Phe Gly 465											1440
ggc cac ccg Gly His Pro											1488
gtt cct gcc Val Pro Ala	-		Leu Le	-	_	-		-	_	-	1536
tac acc aag Tyr Thr Lys 515	Leu Glu										1584
ctt gcg gca Leu Ala Ala 530											1632
gca gca aag Ala Ala Lys 545											1680
gaa cgt gct Glu Arg Ala		Gln Glu									1728
gat gcg att Asp Ala Ile			Ala G								1776
gat gaa gta Asp Glu Val 595	Ala Ala										1824
act gaa tct Thr Glu Ser 610	Asp Ser		Ala Gl		Ala	Ser					1872
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Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly 135 Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val 150 155 Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Asp Pro Val Val 165 170 Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly 180 Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys 200 Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu 295 Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Ser Gln 305 Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn 330 Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg 355 360 365

Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Gln Phe 370 380

Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala 385 390 395 400

Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe 405 415

Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu 420 425 430

Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu 435 440 445

Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu 450 455 460

His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val 465 470 475 480

Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr $485 \hspace{1cm} 490 \hspace{1cm} 495$

Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp 500 505 510

Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu 515 520 525

Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala 530 540

Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala 545 550 555

Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala 565 570 575

Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln 580 585 590

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<220>

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gac cgc gat Asp Arg Asp			Val E								816
gat gac tgg Asp Asp Trp 275	Asp Phe										864
ggc gat gcc Gly Asp Ala 290	_		_	_		-				-	912
gac tcc ttc Asp Ser Phe 305											960
aat ctc cct Asn Leu Pro											1008
acc acc gaa Thr Thr Glu			Pro I								1056
ggc gga acc Gly Gly Thr 355	Ile Thr	•	_	-			_	-	_	_	1104
gtg gag gct Val Glu Ala 370											1152
aag cgt gag Lys Arg Glu 385	_		-	-	-	-	-		_	-	1200
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ctc cac ctt Leu His Leu			Ala S								1296
cat caa cac His Gln His 435	Gly Ala										1344
caa gag ctg Gln Glu Leu 450											1392
gac acc gag	cct dac	act gaa	tct c	gac tcc	gag	cag	gct	gag	gta	gct	1440

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cgc 1496

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<400> 366

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Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln 20 25 30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp 35 40 45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr 50 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly
65 70 75 80

Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser 85 90 95

Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe 100 105 110

Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn 115 120 125

Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser 130 135 140

His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro 145 150 155 160

Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr 165 170 175

Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met 180 185 190

Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu 195 200 205

Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val 210 215 220

Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe 225 230 235 240

Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg

250 255 245 Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln 265 Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn 280 Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe 310 Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln 360 Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu 375 380 Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg 385 390 Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala 405 410 Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala 425 His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro 435 Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala

485 490

Ser Glu Glu Pro Glu Ala Asp Glu Glu Lys

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(547)

<223> RXA01111

<400> 367

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gag cac tcg tac ca Glu His Ser Tyr Gl 1	n Val Trp Pro Gly		Pro Leu G	
acc tat gac ggt gc Thr Tyr Asp Gly Al 25	t gga acg aac tto a Gly Thr Asn Pho 30	e Ala Leu Phe	tcc gac g Ser Asp V	tt gca 211 al Ala
gag cgt gtt gag ct Glu Arg Val Glu Le 40				
att cca ctc gaa ga Ile Pro Leu Glu Gl 55				
ggc gtt caa cct gg Gly Val Gln Pro Gl 70				
aac cca gat gag gg Asn Pro Asp Glu Gl 9	y Lys Arg Cys Ası		Leu Leu V	
ccc tat gct cgt gc Pro Tyr Ala Arg Al 105		Phe Asp Gly		
ttt tct tac gac at Phe Ser Tyr Asp Il 120				
gaa gac agc att ga Glu Asp Ser Ile As 135	t cac aca atg aad p His Thr Met Lys 140	g tct gtc gtg s Ser Val Val 145	gtg aac c Val Asn P	ca ttc 547 ro Phe
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Tyr Pro Leu Gly Se	r Thr Tyr Asp Gl	· -	Asn Phe A	la Leu
Phe Ser Asp Val Al 35	a Glu Arg Val Glu 40	ı Leu Cys Leu	Leu Asp A 45	la Asp
Asn Asn Glu Thr Ar 50	g Ile Pro Leu Glo 55	ı Glu Arg Asp 60	Ala His I	le Trp
His Cys Tyr Leu Pr 65	o Gly Val Gln Pro 70	o Gly Gln Arg 75	Tyr Gly P	he Arg 80

Val His Gly Pro Trp Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn . 90 85 Lys Leu Leu Val Asp Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr Glu Asp Ser Ile Asp His Thr Met Lys Ser Val 135 Val Val Asn Pro Phe 145 <210> 369 <211> 1635 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1612) <223> RXN01550 <400> 369 ttcgccagca gtacttcttc acctctgctt ccctgcaggc catgattcag ggccacctgg 60 115 cgcaccacaa ggacctcagc aactttgccg agttcactcc gtg cag ctc aat gac Val Gln Leu Asn Asp 1 act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp 10 gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr ttc gca tac acc aac cac acc gtg ctc acc gaa gct ctt gag cag tgg 259 Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp 40 307 gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile 55 355 aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu 70 75 403 gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val 100 90 451 cat atq qca tqq att qcc tqt tac qcg qca tat tcc atc aat ggc gtg His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val 105 110

					gag Glu											499
					gag Glu											547
					cgc Arg 155											595
	_				tcc Ser	-	-		-		-		-		_	643
					tat Tyr											691
_	_		-	_	gct Ala		-		_		_					739
					gag Glu											787
					gag Glu 235											835
					ttc Phe											883
	-	-		_	atc Ile			_	-	_		-			-	931
_	Āla		Álá	Ile	atc Ile	Lys	Leu	Ile	Asn	Ser	Ile	Āla	Asp	-	_	979
					gtc Val											1027
					cct Pro 315											1075
					acc Thr											1123
					aac Asn											1171

gcc a													Ala			1219
ttc q	ggt Gly 375	gct Ala	cgc Arg	gtg Val	gaa Glu	gaa Glu 380	ttg Leu	cca Pro	gcc Ala	ctg Leu	cgc Arg 385	gaa Glu	agc Ser	tac Tyr	gag Glu	1267
cca t Pro 1 390																1315
gcc d Ala 1	ctg Leu	gat Asp	aac Asn	ggc Gly 410	acc Thr	ctc Leu	aac Asn	gac Asp	aac Asn 415	aac Asn	agt Ser	ggt Gly	ttg Leu	ttc Phe 420	tac Tyr	1363
gac (Asp 1																1411
acc f																1459
cgt a																1507
gcc f Ala f 470																1555
atc (-	-		_					-							1603
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<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

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Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
50 . 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg 65 70 75 80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala 265 Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser 280 Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys 295 Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu 310 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu 385

	Leu Asp 405	Ala Leu	Asp F	Asn Gly 410	Thr Le	eu Asn	Asp	Asn 415	Asn	
Ser Gly Leu	Phe Tyr 420	Asp Leu	_	His Ser 425	Leu Il	le His	Gly 430	Tyr	Gly	
Lys Asp Ala 435	Ser Asp	Thr Tyr	Tyr \ 440	Val Leu	Gly As	sp Phe 445	Ala	Asp	Tyr	
Arg Glu Thr 450	Arg Asp	Arg Met 455		Ala Asp		la Ser 60	Asp	Pro	Leu	
Gly Trp Ala 465	Arg Met	Ala Trp 470	Ile A	Asn Ile	Cys G 475	lu Ser	Gly	Arg	Phe 480	
Ser Ser Asp	Arg Thr 485	Ile Arg	Asp T	Tyr Ala 490	Thr G	lu Ile	Trp	Lys 495	Leu	
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	cag ctg									48
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<pre><400> 371 atc ttc caa Ile Phe Gln</pre>	cag ctg Gln Leu 5 ttc cgt Phe Arg 20 cgc atg Arg Met tgt tac Cys Tyr atc atc	ttg gag Leu Glu gct cca Ala Pro gcg gca Ala Ala 55	atc of the total atc of	Val Trp 10 gca gcc Ala Ala 25 cag cgc Gln Arg tcc atc Ser Ile acc ttg	gat gg Asp GJ ggc ac GJy Th aat gg Asn GJ gct ga	ga ctg ly Leu ct gtt hr Val 45 gc gtg ly Val 60 ac tgg	Thr gat Asp 30 cat His gca Ala	Glu 15 gaa Glu atg Met gcg Ala	gag Glu gca Ala ctg Leu	96 144
<pre><400> 371 atc ttc caa Ile Phe Gln 1 gat cgc cgc Asp Arg Arg acc atc gac Thr Ile Asp</pre>	cag ctg Gln Leu 5 ttc cgt Phe Arg 20 cgc atg Arg Met tgt tac Cys Tyr atc atc Ile Ile aag ttc	ttg gag Leu Glu gct cca Ala Pro gcg gca Ala Ala 55 aag gcc Lys Ala 70	atc of the total age of	Val Trp 10 gca gcc Ala Ala 25 cag cgc Gln Arg tcc atc Ser Ile acc ttg Thr Leu act aac	gat	ga ctg ly Leu ct gtt hr Val 45 gc gtg ly Val 60 ac tgg sp Trp	Thr gat Asp 30 cat His gca Ala tac Tyr	Glu 15 gaa Glu atg Met gcg Ala gca Ala	gag Glu gca Ala ctg Leu ctg Leu 80	96 144 192

											gag Glu					384
											gaa Glu 140					432
											atc Ile					480
											gtg Val					528
											ctc Leu					576
			_		_	-	_				gac Asp			-	_	624
											tat Tyr 220					672
			-						_	_	ttg Leu	_			-	720
											gta Val					768
											gat Asp					816
					Lys		Āla	Ser		Thr	tcc Ser	Asn				864
											gac Asp 300					912
											tat Tyr					960
											tac Tyr					1008
				-				_	_	-	ttg Leu	_	-	_	_	1056
aac	ggc	acc	ctc	aac	gac	aac	aac	agt	ggt	ttg	ttc	tac	gac	ctc	aag	1104

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Ly 355 360 365	/s
cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac ta His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Ty 370 375 380	
gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gc Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Al 385 390 395 40	
gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg at Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp I 405 410 415	
aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc ga Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg As 420 425 430	
tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag aa Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Ly 435 440 445	
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	Le
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu I	
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu II 1 5 10 15 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu G	Lu
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu II151015 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu Glu Arg Ileu Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Pro Ileu Gln Arg Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Glu Arg Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Glu Arg Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Glu Arg Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg Met Ala Ileu Asp Gly Thr Val His Met Ala Ileu Asp Arg	lu la
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu I151015 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu Glu Arg Ile Gln Arg Gly Thr Val His Met Ala 35 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala 40 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leg 50 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leg	Lu La eu .
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu II151015Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu	Lu La eu . eu 30
Ile Phe Gln Gln LeuPhe Trp Arg Val Trp Glu Ile Ile Thr Glu II15101015Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu	Lu La eu . eu 30
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu II Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu Glu Arg Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala Asp Glu Asp Glu Glu Glu Arg Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Ala Leg 50 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leg 65 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Ang 90 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leg	lu la eu . eu 80
The Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu II Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu 20 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala 35 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Ala Le 50 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Le 65 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Asp 90 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Le 100 Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leg Leg Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leg Leg Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg Leg Ser Asp Leu Leu Lys Lys Lys Leg	lu la eu . eu 80 eg

Gry	Ile	Glu	Ile	Asp 165	Pro	Glu	Ser	Ile	Phe 170	Asp	Val	Gln	Ile	Lys 175	Arg	
Leu	His	Glu	Tyr 180	Lys	Arg	Gln	Leu	Met 185	Asn	Ala	Leu	Tyr	Val 190	Leu	Asp	
Leu	Tyr	Phe 195	Arg	Ile	Lys	Glu	Asp 200	Gly	Leu	Thr	Asp	Ile 205	Pro	Ala	Arg	
Thr	Val 210	Ile	Phe	Gly	Ala	Lys 215	Ala	Ala	Pro	Gly	Tyr 220	Val	Arg	Ala	Lys	
Ala 225	Ile	Ile	Lys	Leu	Ile 230	Asn	Ser	Ile	Ala	Asp 235	Leu	Val	Asn	Asn	Asp 240	
Pro	Glu	Val	Ser	Pro 245	Leu	Leu	Lys	Val	Val 250	Phe	Val	Glu	Asn	Tyr 255	Asn	
			260			Ile		265					270			
		275			_	Glu	280					285				
Met	Met 290	Asn	Gly	Ala	Leu	Thr 295	Leu	Gly	Thr	Met	Asp 300	Gly	Ala	Asn	Val	
	Ile	Val	Asp	Ser	Val	Gly	Glu	Glu	Asn	Ala	Tyr	Ile	Phe	Gly	Ala	
305					310	: .				315					320	
	Val	Glu	Glu	Leu 325		Àla	Leu	Arg	Glu 330		Tyr	Glu	Pro	Tyr 335	320	•
Arg				325	Pro	Ala Gly	•		330	Ser				335	320 Glu	•
Arg Leu Asn	Tyr Gly	Glu Thr 355	Thr 340 Leu	325 Val Asn	Pro Pro Asp	Gly Asn	Leu Asn 360	Lys 345 Ser	330 Arg Gly	Ser Ala Leu	Leu Phe	Asp Tyr 365	Ala 350 Asp	335 Leu Leu	320 Glu Asp Lys	•
Arg Leu Asn His	Tyr Gly Ser 370	Glu Thr 355 Leu	Thr 340 Leu Ile	325 Val Asn His	Pro Pro Asp Gly	Gly Asn Tyr 375	Leu Asn 360 Gly	Lys 345 Ser Lys	330 Arg Gly Asp	Ser Ala Leu Ala	Leu Phe Ser 380	Asp Tyr 365 Asp	Ala 350 Asp	335 Leu Leu Tyr	320 Glu Asp Lys	
Arg Leu Asn His	Tyr Gly Ser 370	Glu Thr 355 Leu	Thr 340 Leu Ile	325 Val Asn His	Pro Pro Asp Gly	Gly Asn Tyr	Leu Asn 360 Gly	Lys 345 Ser Lys	330 Arg Gly Asp	Ser Ala Leu Ala	Leu Phe Ser 380	Asp Tyr 365 Asp	Ala 350 Asp	335 Leu Leu Tyr	320 Glu Asp Lys	
Arg Leu Asn His Val	Tyr Gly Ser 370 Leu	Glu Thr 355 Leu Gly	Thr 340 Leu Ile Asp	325 Val Asn His	Pro Pro Asp Gly Ala 390	Gly Asn Tyr 375	Leu Asn 360 Gly	Lys 345 Ser Lys	330 Arg Gly Asp	Ser Ala Leu Ala Thr 395	Leu Phe Ser 380 Arg	Asp Tyr 365 Asp	Ala 350 Asp Thr	335 Leu Leu Tyr Met	320 Glu Asp Lys Tyr Ala 400	
Arg Leu Asn His Val 385	Tyr Gly Ser 370 Leu Asp	Glu Thr 355 Leu Gly Tyr	Thr 340 Leu Ile Asp	325 Val Asn His Phe Ser 405	Pro Asp Gly Ala 390 Asp	Gly Asn Tyr 375 Asp	Leu Asn 360 Gly Tyr	Lys 345 Ser Lys Arg	330 Arg Gly Asp Glu Trp 410	Ser Ala Leu Ala Thr 395 Ala	Leu Phe Ser 380 Arg	Asp Tyr 365 Asp Asp	Ala 350 Asp Thr Arg	335 Leu Leu Tyr Met	320 Glu Asp Lys Tyr Ala 400 Ile	

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aac Asn			cac His													672
atc Ile 225	gca Ala	gag Glu	ggc Gly	atg Met	gag Glu 230	tac Tyr	cca Pro	gca Ala	gca Ala	ttc Phe 235	gag Glu	cag Gln	gtt Val	cgt Arg	gcg Ala 240	720
			ttc Phe													768
			gag Glu 260													816
gat Asp	cag Gln	cag Gln 275	ctg Leu	tgc Cys	gtt Val	ggt Gly	gtt Val 280	cca Pro	att Ile	gag Glu	aag Lys	gca Ala 285	ctt Leu	gag Glu	ctt Leu	864
ggt Gly	caa Gln 290	gag Glu	tcc Ser	gat Asp	cca Pro	cac His 295	cgc Arg	ttc Phe	aac Asn	atg Met	gct Ala 300	cat His	atg Met	ggc Gly	ctt Leu	912
cgc Arg 305	gcg Ala	agc Ser	caa Gln	cat His	gct Ala 310	aat Asn	ggc Gly	gtc Val	gca Ala	aag Lys 315	ctt Leu	cat His	ggt Gly	gaa Glu	gta Val 320	960
			atg Met													1008
			ggg Gly 340													1056
			atg Met													1104
Leu		Val	gct Ala	Asp	Ser		Ser	Asn	Pro	Gln	Ala	Val				1152
			aag Lys													1200
			gca Ala													1248
			gcg Ala 420													1296
			gca Ala	_	-	-				_	-	_		_	-	1344
ctg	cgc	aac	cct	gaa	cgc	ctg	cgt	tcc	atc	ttg	ctt	aat	gag	gaa	cgc	1392

Leu Arg 450		Pro	Glu	Arg	Leu 455	Arg	Ser	Ile	Leu	Leu 460	Asn	Glu	Glu	Arg	
cca gtt Pro Val 465	cag Gln	ttc Phe	gtt Val	att Ile 470	gct Ala	ggt Gly	aag Lys	gca Ala	cac His 475	cca Pro	cat His	gac Asp	atg Met	ggt Gly 480	1440
ggc aag Gly Lys	aag Lys	ctc Leu	atg Met 485	cag Gln	gaa Glu	atc Ile	gtc Val	cac His 490	ttc Phe	gct Ala	gat Asp	caa Gln	gct Ala 495	ggt Gly	1488
gtc cgt Val Arc	gac Asp	cgt Arg 500	ttc Phe	ctc Leu	ttc Phe	ctg Leu	cct Pro 505	gat Asp	tac Tyr	gac Asp	atc Ile	aac Asn 510	ctg Leu	gcc Ala	1536
agc tac Ser Tyr															1584
cct cac Pro Glr 530	Ğlu														1632
ggc ctc Gly Leu 545		_				-				-	_	_		_	1680
gag acc Glu Thi															1728
tgc cgc Cys Arc															1776
gaa gtt Glu Val	-	-	_			-	-	-	-					_	1824
gac tgg Asp Trp 610	Leu														1872
gtc acc Val Thr 625															1920
cca acc Pro Thi															1968
gat tad Asp Tyr															2016
aag gto Lys Val															2064
ctt gaa Leu Glu	-	-	-	-	_	-			-			_	_		2112

695 700 690 tto caa got cag goa etc ttt ggt gog etc gga cac aac ggt gac atc 2160 Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile 705 715 2208 gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc 2256 Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc 2304 Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa 2348 Leu Ile Thr Tyr Leu Glu Asn 770 <210> 374 <211> 775 <212> PRT <213> Corynebacterium glutamicum <400> 374 Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser 5 10 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly 25 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro 120 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg 130 Ile Pro Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu 150 155 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Val Arg Ala Val Asn Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gln Pro Glu Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 280 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 310 315 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu 330 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val 340 345 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 360 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu 375 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg 455 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly 485 490

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu 570 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met 615 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala 650 Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu 680 Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile 710 715

Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr

Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala 740 750

Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg 755 760 765

Leu Ile Thr Tyr Leu Glu Asn 770 775

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<211> 941

<212> DNA

<213> Corynebacterium glutamicum

<220>

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Arg Val Asp 225					ttc caa Phe Gln			720
ctc ttt ggt Leu Phe Gly	gcg ctc Ala Leu 245	gga cac Gly His	aac ggt Asn Gly	gac atc Asp Ile 250	gaa gat Glu Asp	cca ga Pro Gl 25	u Ile	768
acc gtt ttg Thr Val Leu								816
act gac ctg Thr Asp Leu 275								864
aac agg atg Asn Arg Met 290								912
gag aac tago Glu Asn 305	ggcgaaa	ctagcttt	ac caa					941
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Gln Glu Ile	Val His	Phe Ala	_	Ala Gly	Val Arg		g Phe	
	20		25			30		
Leu Phe Leu 35		Tyr Asp		Leu Ala	Ser Tyr 45		le Ser	
	Pro Asp		Ile Asn 40 Asn Pro		45	Leu Il		
35 Gly Ala Asp	Pro Asp	Leu Asn 55	Ile Asn 40 Asn Pro	Val Arg	45 Pro Gln 60	Leu II	la Ser	
35 Gly Ala Asp 50 Gly Thr Ser	Pro Asp Val Trp Gly Met	Leu Asn 55 Lys Ala 70	Ile Asn 40 Asn Pro Val Met	Val Arg Asn Gly 75	Pro Gln 60 Gly Leu	Leu II Glu Al Thr Le	la Ser eu Ser 80	
Gly Ala Asp 50 Gly Thr Ser 65	Pro Asp Val Trp Gly Met Gly Trp 85	Leu Asn 55 Lys Ala 70 Trp Asp	Ile Asn 40 Asn Pro Val Met Glu Met	Val Arg Asn Gly 75 Pro Lys 90	Pro Gln 60 Gly Leu Glu Thr	Leu III Glu Al Thr Le	la Ser eu Ser 80 Ly Trp	
Gly Ala Asp 50 Gly Thr Ser 65 Ile Ser Asp	Pro Asp Val Trp Gly Met Gly Trp 85 Thr Val	Leu Asn 55 Lys Ala 70 Trp Asp Glu Ser	Ile Asn 40 Asn Pro Val Met Glu Met Gln Asp	Val Arg Asn Gly 75 Pro Lys 90 Leu Glu	Pro Gln 60 Gly Leu Glu Thr Cys Arg	Leu III Glu AI Thr Le Thr GI Asp Hi	la Ser eu Ser 80 ly Trp 55	
Gly Ala Asp 50 Cly Thr Ser 65 Thr Ile Pro Glu Ser Gln	Pro Asp Val Trp Gly Met Gly Trp 85 Thr Val 100 Ala Leu	Leu Asn 55 Lys Ala 70 Trp Asp Glu Ser Tyr Asp	Ile Asn 40 Asn Pro Val Met Glu Met Gln Asp 105 Leu Leu	Val Arg Asn Gly 75 Pro Lys 90 Leu Glu Glu Asn	Pro Gln 60 Gly Leu Glu Thr Cys Arg Glu Val 125	Leu II Glu Ai Thr Le Thr Gl Asp Hi 110 Ala Pi	la Ser eu Ser 80 ly Trp 55 ls Leu	

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile 250 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser 265 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn 285 280 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu 300 290 295 Glu Asn 305 <210> 377 <211> 1206 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1206) <223> FRXA02113 <400> 377 48 cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser 96 gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly 20 gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser 35 ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met 50 aag tot goa tot gac ttg ggt gtg coa ctg atc ggt gtt ggt ttg ctc Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu 65

tac acc Tyr Thr	cac go His G	gc tac ly Tyr 85	ttc Phe	acc Thr	cag Gln	tca Ser	ctg Leu 90	tcc Ser	ggt Gly	gac Asp	ggt Gly	tgg Trp 95	cag Gln	288
cag gaa Gln Glu	Glu T	ac aag yr Lys 00	tac Tyr	cac His	gat Asp	cca Pro 105	gca Ala	gaa Glu	ctg Leu	ccg Pro	att Ile 110	gag Glu	gca Ala	336
gtt aaa Val Lys	gat a Asp L 115	ag aac ys Asn	ggc Gly	gag Glu	cag Gln 120	gtc Val	act Thr	gtt Val	tct Ser	gtc Val 125	acc Thr	tac Tyr	cca Pro	384
ggt gcg Gly Ala 130	cag g Gln G	aa gta lu Val	aag Lys	att Ile 135	gca Ala	ctg Leu	tgg Trp	gta Val	gca Ala 140	aac Asn	gtt Val	ggc Gly	cgc Arg	432
atc cca Ile Pro 145														480
ctc cgc Leu Arg														528
atc aag Ile Lys	Gln G	aa ctc lu Leu 80	gtt Val	ctc Leu	ggt Gly	gtt Val 185	ggt Gly	ggc Gly	gtc Val	cgc Arg	gct Ala 190	gtc Val	aac Asn	576
gca ttc Ala Phe														624
aac gaa Asn Glu 210														672
atc gca Ile Ala 225														720
tcc aac Ser Asn	atc t Ile P	tc acc he Thr 245	Thr	cac His	Thr	Pro	Val	Pro	Ala	Gly	atc Ile	gac Asp 255	Arg	768
ttc gac Phe Asp	Met G													816
gat cag Asp Gln	cag c Gln L 275	tg tgc eu Cys	gtt Val	ggt Gly	gtt Val 280	cca Pro	att Ile	gag Glu	aag Lys	gca Ala 285	ctt Leu	gag Glu	ctt Leu	864
ggt caa Gly Gln 290														912
cgc gcg Arg Ala 305	agc c Ser G	aa cat In His	gct Ala 310	aat Asn	ggc Gly	gtc Val	gca Ala	aag Lys 315	ctt Leu	cat His	ggt Gly	gaa Glu	gta Val 320	960

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu 325 330 335	1008
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val 340 345 350	1056
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 355 360 365	1104
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu 370 375 380	1152
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val 385 390 395 400	1200
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Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser 10	
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Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg Ile Lys Gln Glu Leu Val Leu Gly Val Gly Val Arg Ala Val Asn Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu 200 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 215 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 235 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gln Pro Glu Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 280 275 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 310 315 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 360 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val 395 Ala Arg <210> 379 <211> 1140 <212> DNA <213> Corynebacterium glutamicum <220>

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tgg gtg agc gtt gtg Trp Val Ser Val Val 10	gcg tca tgt gtt atc g Ala Ser Cys Val Ile <i>l</i> 15	gca agc acg ctg Ala Ser Thr Leu	att ctg 163 Ile Leu 20
gtg cct tcg cat tcc Val Pro Ser His Ser 25	ggt gcg gag gaa gtc g Gly Ala Glu Glu Val A 30	gat caa ctg att Asp Gln Leu Ile 35	gct gat 211 Ala Asp
	cag gaa acg tct gcc o Gln Glu Thr Ser Ala (45		
	att gag gct cgt gag g Ile Glu Ala Arg Glu V 60		
	agc tac cgt gag gcg g Ser Tyr Arg Glu Ala A 75		
	cgt tcg gag atc aat o Arg Ser Glu Ile Asn A 95		
	acg gat cct ttg agc a Thr Asp Pro Leu Ser 1 110		
	att gat cgg atg agc t Ile Asp Arg Met Ser 1 125		
	gtg gtt gaa tcc ctc a Val Val Glu Ser Leu A 140		
	tat caa gca aac cgt a Tyr Gln Ala Asn Arg 1 155	Thr Lys Ala Glu	
	ctg aag gta cgc cag g Leu Lys Val Arg Gln <i>P</i> 175		
	ggt cga aaa tcg gag a Gly Arg Lys Ser Glu 1 190		
	gag cgg gaa atg tgg g Glu Arg Glu Met Trp V 205		
	act gat ttg ctt ggt o Thr Asp Leu Leu Gly I 220		

ggt gcg gtg Gly Ala Val 230											835
ggt ggc att Gly Gly Ile											883
gcg tat cag Ala Tyr Gln				ı Pro							931
atg gct ggc Met Ala Gly 280											979
gtc att gga Val Ile Gly 295											1027
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Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn

135 Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr 150 155 Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile 180 185 Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val 200 Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu 215 Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val 295 300 Gly Leu Tyr Ile Gly Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly 305 Ile Pro Val Gln Val Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala 330 325 Arg Arg Tyr <210> 381 <211> 1959 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1936) <223> RXA01478 <400> 381 qcqqqttttq ttqtqqaggq qcqcqtcqaa aagcaatttt ttttccaaga tagctcactt 60 tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga Met Thr Ile Pro Gly 1 qct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac

Ala Ser	Thr	Gln	Thr 10	Asp	Ile	Pro	Leu	Asp 15	Thr	Leu	Leu	Glu	Asp 20	Tyr	
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agt ttg Ser Leu															259
acc agg Thr Arg 55															307
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cgc tct Arg Ser															499
cgc ctg Arg Leu 135	Arg														547
act gtc Thr Val 150															595
gta tat Val Tyr															643
cac agt His Ser		Thr													691
		185					190	-		501		195			
ctc acc Leu Thr		gca					ccg	cat	ccc	ccc	atg	195 ccg			739
	Trp 200 tct Ser	gca Ala ttg	Pro	Ser	Phe acc	Glu 205 ttg	ccg Pro	cat His	ccc Pro	ccc Pro gca	atg Met 210 tca	195 ccg Pro	Asp	Tyr gaa	739 787
Leu Thr acc cgc Thr Arg	Trp 200 tct Ser	gca Ala ttg Leu	Pro gag Glu cag	Ser agc Ser	Phe acc Thr 220 ctc	Glu 205 ttg Leu tac	ccg Pro agc Ser	cat His ttc Phe	ccc Pro tgg Trp	ccc Pro gca Ala 225	atg Met 210 tca Ser	195 ccg Pro tgg Trp	Asp gtt Val tcc	Tyr gaa Glu atg	

	250		:	255		260		
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gac tac cg Asp Tyr Ar 28	g Tyr Val	Trp Leu A					J	979
ctc gtg ga Leu Val Gl 295				Ala Leu				1027
ctg ctg cg Leu Leu Ar 310	-	gca ggc ga Ala Gly As 315	-	-	-	_		1075
ggc ctc gg Gly Leu Gl			eu Pro					1123
cgc gga ta Arg Gly Ty					Gly Asn		_	1171
gaa caa ta Glu Gln Ty 36	r Gln Ala	Asp Val Va						1219
acc atc cg Thr Ile Ar 375		ggg tgc ct Gly Cys Le 380		Asp Glu			_	1267
caa aaa gc Gln Lys Al 390		gat ttc ca Asp Phe GI 395					_	1315
caa ggc at Gln Gly Il			er Glu				22	1363
		gcc ggc tt Ala Gly Ph			Ile Lys			1411
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		atc atg ad Ile Met Th 460		Gly Phe				1507
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Glu	Leu	Gln	His 340	Leu	Arg	Gly	Tyr	Glu 345	Asn	Ser	Val	Pro	Val 350	Arg	Val
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Ile	Lys	Ala	Ile	Glu	Glu	Phe	Asn 440	Leu	Asp	Gly	Pro	Ile 445	Glu	Arg	Trp

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75

Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr

Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr

85 90 95 Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr 125 120 Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu 150 155 Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile 170 Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu 180 185 <210> 385 <211> 1503 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1480) <223> RXN01927 <400> 385 gagcagcggg atcttttgcg taattcgcgc gcgcagatcc atgtgattga ccacaatggt 60 gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt 115 Met Ala Leu Val Leu 1 gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163 Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala 10 211 gee ace gge cag gtt ate gae gaa gge ege geg agt cae eeg age ggg Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly 25 259 tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr 40 gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307 Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln 55 cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala 75 70 403 ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat

95

100

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90

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tat Tyr	gtt Val	gct Ala 120	tct Ser	tta Leu	act Thr	gcc Ala	acc Thr 125	aaa Lys	atg Met	cgg Arg	tgg Trp	atg Met 130	cgt Arg	gat Asp	cat His	499
gaa Glu	cca Pro 135	gaa Glu	aat Asn	gca Ala	gcg Ala	cgc Arg 140	acg Thr	gcg Ala	tcg Ser	gtg Val	atg Met 145	ttg Leu	cct Pro	cat His	gat Asp	547
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	gat Asp															643
	acc Thr															691
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	gtt Val 215															787
	ttg Leu															835
	ggc Gly															883
	ggt Gly								Tyr			Leu		Cys		931
	aat Asn															979
	tgg Trp 295															1027
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Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala

Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser

Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu

Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala

Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp

Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg

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Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg 145 150 155 160

Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr 165 170 175

Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His 180 185 190

Glu Val Glu Leu Pro Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr 195 200 205

Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala 210 215 220

Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile
225 230 235 240

Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255$

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Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg 275 280 285

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Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala 290 295 300

Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly 305 310 315 320

Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu
325 330 335

Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly 340 345 350

Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr 355 360 365

Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser 370 375 380

Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val 385 390 395 400

Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala 405 410 415

Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro 420 425 430

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gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc

576

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gca cgt ggc Ala Arg Gly												768
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ctc atc ggt Leu Ile Gly 290			g Ser									912
gag att ttc Glu Ile Phe 305												960
gcg ttg ggt Ala Leu Gly												1008
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140

547

120

135

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gtg a Val I																643
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Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val 50 60

Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu 65 70 75 80

Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val\$85\$ 90 95

Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu 100 105 110

Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu 115 120 125

Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu

130 135 140 Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu 155 Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly 170 His Asp Gln Leu Arq Arq Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro Thr Pro Lys 245 <210> 391 <211> 1026 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1003) <223> RXA02797 <400> 391 acaqtctcat qaaqccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60 ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att Met Asn Asn Arg Ile gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163 Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg cac cca gca cct ggc gaa aca ctg ttg ggc agt gga cac atc act His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259 Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly 45 qca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307 Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala 355 cca gcc tta gaa ttc ctt cgt tcg tca ggc gtc gac ctt acg gca gta Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val 75 80

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Asp Gly Glu	aac aat atc o Asn Asn Ile V 105					451
	tat gta agc a Tyr Val Ser S					499
	ctg caa ggt c Leu Gln Gly G		Ala Asp G			547
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	aag tcc gcg t Lys Ser Ala I 170					643
Glu His Glu	gcc ggc ctg a Ala Gly Leu 1 185					691
	ccc cac gag o Pro His Glu I					739
	gtt tta acg o Val Leu Thr I 2		Ala Gly A			787
	atc acg gac a Ile Thr Asp 1 235					835
	gcc ggt gac o Ala Gly Asp A 250	Ala Phe Ala				883
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Gly Gly His Ile Th $\hat{\mathbf{r}}$ Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala 35 40

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys 50 55 60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val 65 70 75 80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val 85 90 95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly 100 105 110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu 115 120 125

Leu Ala Glu Ala Gly Ile Leu Leu Gln Gly Glu Ile Pro Ala Asp 130 135 140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn 150 155 160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp 165 170 175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe 180 185 190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu 195 200 205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly 210 215 220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr 225 230 235 240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala 245 250 255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr 260 265 270

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Ser	Leu	Glu 115	Phe	Leu	Thr	Ser	His 120	Gly	Val	Asp	Gly	Ile 125	Ile	Cys	Val
Pro	Asn 130	Glu	Glu	Cys	Ala	Asn 135	Gln	Leu	Glu	Asp	Leu 140	Gln	Lys	Gln	Gly
Met 145	Pro	Val	Val	Leu	Val 150	Asp	Arg	Glu	Leu	Pro 155	Gly	Asp	Ser	Thr	Ile 160
Pro	Thr	Ala	Thr	Ser 165	Asn	Pro	Gln	Pro	Gly 170	Ile	Ala	Ala	Ala	Val 175	Glu
			180		Asn			185		_	_		190		
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~	- 1	•	~	_			~ 3	~ 1	_		D1.	-	~ 1	01	m
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Glu 225 Ala Glu Ile	210 Gln Lys Ala Gly	Ser Thr Cys Phe 275	Val Leu His 260 Asp	Gly Phe 245 Lys	Phe 230 Ala Ala	Glu Gly Gly Pro	Gly Asp Leu Leu 280	Ala Ser Val 265 Phe	Thr Met 250 Ile Ala	Lys 235 Met Gly	220 Leu Thr Lys Gln	Leu Ile Asp Pro 285	Asp Gly Val 270 His	Gln Val 255 Ser Pro	Gly 240 Ile Val Leu
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Glu 225 Ala Glu Ile Thr	210 Gln Lys Ala Gly Val 290 Leu	Thr Cys Phe 275 Ile	Val Leu His 260 Asp Asp	Gly Phe 245 Lys Thr Gln Leu	Phe 230 Ala Ala His Asn	Gly Gly Pro Val 295 Ala	Gly Asp Leu Leu 280 Glu	Ala Ser Val 265 Phe Gln	Thr Met 250 Ile Ala Leu Val	Lys 235 Met Gly Leu Ala Pro 315	220 Leu Thr Lys Gln Gln 300 Ser	Leu Ile Asp Pro 285 Arg	Asp Gly Val 270 His Ala	Gln Val 255 Ser Pro Val Lys	Gly 240 Ile Val Leu Ser Thr 320

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50 55 60 Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala 105 Thr Asn Gly Glu Ser Leu Glu Ser 115 <210> 397 <211> 795 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(772) <223> RXA01325 <400> 397 qcqcaqcqct cqqacqatta cqaacttcag gagaactcgg ggtcattcgt tgcattctac 60 cctggaaatt ttcccacact aagtcaggtc taagtagggt atg gat atg acg att 115 Met Asp Met Thr Ile 1 tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163 Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro 15 20 10 gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu 25 ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr 40 gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307 Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe 55 355 ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu 70 403 gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Leu Asp Ile Ala 90 451 gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala 105 110 115

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499

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95

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355

403

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cac tet gec His Ser Ala 150												595
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140

135

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									ggt Gly 175							643
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Leu	Pro	Ile	Ala	Leu 85	Ala	Leu	Asp	Trp	Pro 90	His	Arg	Val	Pro	Lys 95	Ala	
Gln	Pro	Ala	Leu 100	Asp	Phe	Thr	Ala	Ala 105	His	Thr	Trp	Ala	Phe 110	Glu	Pro	
Val	Asp	Asp 115	Ala	Ala	Phe	Pro	Ala 120	Val	Gln	Leu	Ala	Arg 125	His	Val	Ala	
Lys	Gln 130	Lys	Gly	Thr	Tyr	Pro 135	Ala	Val	Tyr	Asn	Ala 140	Ala	Asn	Glu	Glu	
Ala 145	Ala	Glu	Ala	Phe	Leu 150	Arg	Gly	Arg	Ile	Lys 155	Phe	Pro	Gln	Ile	Val 160	
Asp	Val	Val	Asp	Glu 165	Val	Leu	Gln	Gly	Ala 170	Ser	Gln	Phe	Ala	Gly 175	Val	
Ala	Ser	His	Val 180	Asp	Asp	Ile	Leu	Ala 185	Thr	Glu	Ser	Glu	Ala 190	Arg	Ala	
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agt att tca aca cct Ser Ile Ser Thr Pro 10	Ala Asp Leu Lys			163
gac gct ctt gcc aaa Asp Ala Leu Ala Lys 25		Phe Leu Val		211
gca act ggt ggc cac Ala Thr Gly Gly His 40				259
atc ggt ctt cat cga Ile Gly Leu His Arc 55				307
gat act tct cac cac Asp Thr Ser His Glr 70				355
aaa gat ttt gat tot Lys Asp Phe Asp Ser 90	Leu Arg Gln Lys			403
tgc cgt gct gaa agt Cys Arg Ala Glu Ser 105		Thr Glu Ser		451
gcg gcc ttg tct tat Ala Ala Leu Ser Tyr 120	geg gat ggt ttg Ala Asp Gly Led 125	tct aaa gcc Ser Lys Ala	aag cag ttg gat Lys Gln Leu Asp 130	499
ggc gat acc acg cat Gly Asp Thr Thr His 135				547
act ggc ggc atg tgt Thr Gly Gly Met Cys 150				595
gac cgc aaa gtt gtt Asp Arg Lys Val Val	gtc gta gtc aat Val Val Val Asn	gac aat ggc Asp Asn Gly	cgg agt tat tct Arg Ser Tyr Ser	643

	170	175		180
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cct ttc tat gat Pro Phe Tyr Asp 200	Arg Phe Met	gaa aag ggc Glu Lys Gly 205	aag acg tcc ctg Lys Thr Ser Leu 210	aaa tcc 739 Lys Ser
atg ggg tgg gta Met Gly Trp Val 215	ggg gag cgt Gly Glu Arg 220	act ttt gaa Thr Phe Glu	gcg ctc cat gca Ala Leu His Ala 225	ttt aaa 787 Phe Lys
gaa ggt gtg aag Glu Gly Val Lys 230	agc acc gtc Ser Thr Val 235	att ccc acc Ile Pro Thr	gaa atg ttc cct Glu Met Phe Pro 240	gaa ctg 835 Glu Leu 245
			cat aac caa aaa His Asn Gln Lys	
gac aat gcg ctg Asp Asn Ala Leu 265			gat ggc ccc ato Asp Gly Pro Ile 275	Ile Val
	Glu Lys Gly		gcg cct gct gag Ala Pro Ala Glu 290	
			atc gat ccg ctc lle Asp Pro Leu 305	
			acc tct gtg ttc Thr Ser Val Phe 320	
gag ctg gtc aag Glu Leu Val Lys			Asn Val Val Ala	
			aag ttc gaa gcc Lys Phe Glu Ala 355	Asn Phe
	Phe Asp Val		gag cag cac gcg Glu Gln His Ala 370	
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			cag ctg ctc atg Gln Leu Leu Met 400	
			ctt gat cgc tca Leu Asp Arg Ser	

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						gtg Val										1459
tcc Ser	ttg Leu 455	cgt Arg	gag Glu	ctg Leu	ctc Leu	aat Asn 460	gag Glu	gct Ala	att Ile	tcc Ser	atc Ile 465	gat Asp	gat Asp	ggc Gly	ccc Pro	1507
						aag Lys										1555
atc Ile	gac Asp	acc Thr	ttg Leu	gaa Glu 490	gac Asp	ggc Gly	gtg Val	gat Asp	gtc Val 495	ctc Leu	gca Ala	tat Tyr	gaa Glu	gac Asp 500	gcc Ala	1603
Thr	Āsp	Val	Glu 505	Ser	Thr	gac Asp	Asp	Ala 510	Pro	Ser	Val	Leu	Ile 515	Ile	Ala	1651
Val	Gly	Glu 520	Arg	Ala	Thr	gtt Val	Ala 525	Leu	Asp	Val	Ala	Ser 530	Arg	Ile	Lys	1699
cag Gln	cac His 535	ggc Gly	gtg Val	aac Asn	gtc Val	acg Thr 540	gtt Val	gtt Val	gac Asp	ccc Pro	cgc Arg 545	tgg Trp	att Ile	gtc Val	ccc Pro	1747
						gcg Ala										1795
						atc Ile										1843
		Leu		Ala		gag Glu		Asp	Thr	Pro	Arg	Arg		Ile		1891
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Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln 50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu 100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn 165 170 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala 180 185 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys 195 200 205

Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala 210 215 220

Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu 225 230 235 240

Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His 245 250 255

Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp 260 265 270

Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala 275 280 285

Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile 290 295 300

Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr

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Ser Val Phe Ser	Asp Glu Leu 325	Val Lys Ile 330	Gly Ala Gln	Asn Glu Asn 335
Val Val Ala Ile 340	Thr Ala Ala	Met Ala Gly 345	Pro Thr Gly	Leu Ser Lys 350
Phe Glu Ala Asn 355	Phe Pro Asn	Arg Phe Phe 360	Asp Val Gly 365	Ile Ala Glu
Gln His Ala Val 370	Thr Ser Ala 375	Ala Gly Leu	Ala Leu Gly 380	Gly Lys His
Pro Val Val Ala 385	Ile Tyr Ser 390	Thr Phe Leu	Asn Arg Ala 395	Phe Asp Gln 400
Leu Leu Met Asp	Val Gly Met 405	Leu Asn Gln 410	Pro Val Thr	Leu Val Leu 415
Asp Arg Ser Gly 420	Val Thr Gly	Ser Asp Gly 425	Ala Ser His	Asn Gly Val 430
Trp Asp Met Ala 435	Leu Thr Ser	Ile Val Pro 440	Gly Val Gln 445	Val Ala Ala
Pro Arg Asp Glu 450	Asp Ser Leu 455	Arg Glu Leu	Leu Asn Glu 460	Ala Ile Ser
Ile Asp Asp Gly 465	Pro Thr Val	Val Arg Phe	Pro Lys Gly 475	Asp Leu Pro 480
Thr Pro Ile Val	Ala Ile Asp 485	Thr Leu Glu 490	Asp Gly Val	Asp Val Leu 495
Ala Tyr Glu Asp 500	Ala Thr Asp	Val Glu Ser 505	Thr Asp Asp	Ala Pro Ser 510
Val Leu Ile Ile 515	Ala Val Gly	Glu Arg Ala 520	Thr Val Ala 525	Leu Asp Val
Ala Ser Arg Ile 530	Lys Gln His 535	Gly Val Asn	Val Thr Val 540	Val Asp Pro
Arg Trp Ile Val 545	Pro Ile Pro 550	Gln Ser Leu	Val Ala Leu 555	Ser Asp Asp 560
His Asp Leu Val	Ile Thr Ile 565	Glu Asp Gly 570	Val Ile His	Gly Gly Val 575
Gly Ser Leu Leu 580	Ser Asp Ala	Leu Asn Ala 585	Ser Glu Val	Asp Thr Pro 590
Arg Arg Gln Ile 595	Ala Val Pro	Gln Lys Tyr 600	Leu Asp His 605	Ala Ser Arg
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Thr Val Val Gly 625	Trp Leu Asp 630	Ser Leu Phe	Gly Glu 635	

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						tct Ser						96
						aag Lys						144
						gca Ala 55						192
						ttc Phe						240
						ggc Gly						288
						ttc Phe						336
						aac Asn						384
						gat Asp 135						432
						gtt Val						480
						gag Glu						528
						cgt Arg						576

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gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu 210 215 220	672
atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser 225 230 235 240	720
agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp 245 250 255	768
att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp 260 265 270	816
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Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val 35 40 45	

PCT/IB00/00943 WO 01/00844

Ala 65	Asn	Phe	Pro	Asn	Arg 70	Phe	Phe	Asp	Val	Gly 75	Ile	Ala	Glu	Gln	His 80
Ala	Val	Thr	Ser	Ala 85	Ala	Gly	Leu	Ala	Leu 90	Gly	Gly	Lys	His	Pro 95	Val
Val	Ala	Ile	Tyr 100	Ser	Thr	Phè	Leu	Asn 105	Arg	Ala	Phe	Asp	Gln 110	Leu	Leu
Met	Asp	Val 115	Gly	Met	Leu	Asn	Gln 120	Pro	Val	Thr	Leu	Val 125	Leu	Asp	Arg
Ser	Gly 130	Val	Thr	Gly	Ser	Asp 135	Gly	Ala	Ser	His	Asn 140	Gly	Val	Trp	Asp
Met 145	Ala	Leu	Thr	Ser	Ile 150	Val	Pro	Gly	Val	Gln 155	Val	Ala	Ala	Pro	Arg 160
_		_		165		Glu			170					175	
	_		180			Arg		185					190		
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		_		245		Val			250					255	
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		275				Asp	280					285			
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305					310	Lys				315					320
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Met Gly Ile Leu Asn
1 5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg $$ 163 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu $$ 10 $$ 15 $$ 20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca $\,$ 211 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala $\,$ 25 $\,$ 30 $\,$ 35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc $$ 259 Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr $$ 40 $$ 45 $$ 50

atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307 Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe 55 60 65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
70 75 80 85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc $$ 403 Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr $$ 95 $$ 100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg

Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser

105

110

115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
120 125 130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547 Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu 135 140 145

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Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
150 160 165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643 Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser 170 175 180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691 Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln 185 190 195

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Pro Phe Tyr Asp

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Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln 50 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly 85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
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Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Asn Asp Asn 165 170 175

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	gcc cat att gag Ala His Ile Glu			
	ctg ggt gtg aat Leu Gly Val Asn 45			
	caa cgc caa att Gln Arg Gln Ile 60			
	cct cca tcg gtg Pro Pro Ser Val 75			
	cat gtg cac gac His Val His Asp 90			
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	gaa att gat ggg Glu Ile Asp Gly 125			
	gat ctc ccc ttg Asp Leu Pro Leu 140			
	tca gct gag tgc Ser Ala Glu Cys 155		Ile Thr Pro	
	gat aag tat ctt Asp Lys Tyr Leu 170			
	tct gtg cgt tcc Ser Val Arg Ser			Gly Asp
	gga aac ttg gca Gly Asn Leu Ala 205			
	atc aac ccc atg lile Asn Pro Met 220			

	gag Glu															835
	tac Tyr															883
	cta Leu															931
	ctg Leu															979
	caa Gln 295															1027
	gcc Ala															1075
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	cac His															1171
	ttg Leu														cgc Arg	1219
	gtc Val 375															1267
ggt Gly 390	gtg Val	cat His	cca Pro	ggt Gly	ggt Gly 395	gct Ala	gat Asp	gcc Ala	Gln	aac Asn 400	Leu	agc Ser	cac His	gta Val	ctt Leu 405	1315
	ccg Pro															1363
	caa Gln															1411
-	ggc Gly			_		-		_	_	-		-	_	_		1459
	ggc Gly 455															1507
gtc	atg	cca	cgc	atg	caa	tcc	cct	gct	acg	ggc	acc	tat	atc	cgc	ttc	1555

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ggc gcc gtt gtc Gly Ala Val Val 505					1651
caa gat gca ttg Gln Asp Ala Leu 520					1699
ttc gag cat tcc Phe Glu His Ser 535					1747
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gct ggt tat ttg Ala Gly Tyr Leu	gag ggc gag Glu Gly Glu 570	cac att gct His Ile Ala 575	ctt cgt gag Leu Arg Glu	cga ttg ggg Arg Leu Gly 580	1843
gtg ctc aac act Val Leu Asn Thr 585					1891
caa gcg gag atc Gln Ala Glu Ile 600					1939
cgg gaa tac gtg Arg Glu Tyr Val 615					1987
ctg ttg gaa ggc Leu Leu Glu Gly 630					2035
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cag ccg ggc aca Gln Pro Gly Thr 665					2131
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Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe 50 55 60

His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val 65 70 75 80

Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro 85 90 95

Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser 100 105 110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp 115 120 125

Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His 130 135 140

Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile 145 150155155160

Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro 165 170 175

Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser 180 185 190

Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val 195 200 205

Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala 210 215 220

Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg 225 230 235 240

Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe 245 250 255

Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala 260 265 270

Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp 275 280 285

Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu 315 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro 425 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg 440 Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly 465 470 475 Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His 555 Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala 585 Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg

615 620 610 Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys 635 630 Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu 650 Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu 680 Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys 695 Arg Asp 705 <210> 411 <211> 2223 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2200) <223> FRXA00879 <400> 411 aaaagatgta ttttctaaca aacttaccct cacgctacaa atatgctgtg cccacacgct 60 attagtggca taatgttgtg ttgtgactgc tcgcagattt ttg aat gaa ctc gcc 115 Leu Asn Glu Leu Ala 1 gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat 163 Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His 10 att qaq qtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly 25 30 35 gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc 259 Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg 40 307 caa att qcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro 55 60 tcq gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg 355 Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val 70 75 403 cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr 90 95

cag Gln	cgg Arg	gat Asp	gtt Val 105	tct Ser	cag Gln	gtg Val	gaa Glu	aac Asn 110	tgg Trp	aca Thr	gcg Ala	cca Pro	cgg Arg 115	gaa Glu	att Ile	451
gat Asp	ggg Gly	att Ile 120	agg Arg	tgg Trp	ggc Gly	gag Glu	gca Ala 125	tcg Ser	ttt Phe	aag Lys	att Ile	cct Pro 130	ggt Gly	gat Asp	ctc Leu	499
								ctt Leu								547
gag Glu 150	tgc Cys	ggt Gly	ttg Leu	atc Ile	atc Ile 155	acc Thr	ccg Pro	gct Ala	cgt Arg	ctg Leu 160	tct Ser	act Thr	gct Ala	gat Asp	aag Lys 165	595
								gtc Val								643
cgt Arg	tcc Ser	acg Thr	ttg Leu 185	tcg Ser	tgg Trp	ggc Gly	atg Met	ggt Gly 190	gat Asp	ttc Phe	aat Asn	gat Asp	tta Leu 195	gga Gly	aac Asn	691
								gga Gly								739
								cct Pro								787
								aac Asn								835
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								gca Ala								979
								gaa Glu								1027
								ctt Leu								1075
								gaa Glu								1123

						atg Met										1171
						gct Ala										1219
						gac Asp 380										1267
						agc Ser										1315
						tac Tyr										1363
						cgt Arg										1411 .
						gtg Val										1459
						ttc Phe 460										1507
						tat Tyr										1555
						gca Ala										1603
				Thr		gag Glu	Pro		Val			Ala		Ala		1651
						tcg Ser										1699
						cag Gln 540										1747
						ctc Leu										1795
						gag Glu										1843
gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	caa	gcg	gag	atc	ctt	gat	1891

Ala Ala Glu	Leu Al 585	a Glu	Asp	Leu	Gln 590	Trp	Gln	Ala	Glu	Ile 595	Leu	Asp	
gtc gca gca Val Ala Ala 600	Ser Al												1939
gaa cgc gat Glu Arg Asp 615	cag cg Gln Ar	c ggt g Gly	gag Glu 620	ttg Leu	gct Ala	gag Glu	ctg Leu	ttg Leu 625	gaa Glu	ggc Gly	ctg Leu	cac His	1987
act ttc gtt Thr Phe Val 630	gcg aa Ala Ly	a acc s Thr 635	cct Pro	tca Ser	gca Ala	ctg Leu	acc Thr 640	tgt Cys	gtc Val	tgc Cys	ttg Leu	gta Val 645	2035
gac atg gtc Asp Met Val		ı Lys											2083
gat atg tat Asp Met Tyr													2131
tcc gtg ctc Ser Val Leu 680	Ile Gl												2179
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Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp 200 Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr 215 Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile 230 235 Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp 250 Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn 260 Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp 315 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp 345 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser 440

Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val 450

Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp 460

480

His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly 485 490 495

Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln 500 505 510

Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe 515 520 525

Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg 530 535 540

Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala 545 550 555 560

Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val 565 570 575

Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln 580 585 590

Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg 595 600 605

Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu 610 615 620

Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr 625 630 635 640

Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln 645 650 655

Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys 660 665 670

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Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp 690 695 700

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXN00043

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His Tyr Gln Glu A	at gca ggt caa gca sn Ala Gly Gln Ala 10		Ile Glu G	
	ac ggg gtg att gat is Gly Val Ile Asp 30			
	aa ctc tct gga gaa lu Leu Ser Gly Glu 45			
_	tc ccc acg att gtt eu Pro Thr Ile Val 60	_	_	
	ac ggt ggc gcg ttt sn Gly Gly Ala Phe 75			
Ala Arg Asn Ala A	cg cag tat cac cgc la Gln Tyr His Arg 90		Thr Thr V	
	tt tcg gcg ccg gct al Ser Ala Pro Ala 110			
-	cc ttg tgt gaa gag ro Leu Cys Glu Glu 125			
	tc atc aac gca tgc he Ile Asn Ala Cys 140			
-	cc ggc aac cca aca ro Gly Asn Pro Thr 155	•		
Ala Gly Lys Gly T	gg atc aaa tcg atc rp Ile Lys Ser Ile 70		Pro Glu T	
	tt ctc gat ctc tgc eu Leu Asp Leu Cys 190			_
	ct gat gca gat ttt hr Asp Ala Asp Phe 205			
	ag aaa aat gtg acg lu Lys Asn Val Thr 220			

aat gcg atg cct Asn Ala Met Pro 230			• • •		-
ttg ctt gct gcg Leu Leu Ala Ala					
gac ggc gtg cat Asp Gly Val His 265					
aac gcc ttt ttc Asn Ala Phe Phe 280		-			
ggt gag tac att Gly Glu Tyr Ile 295		Leu Asn Val	-		-
gcc cgt ctg cgc Ala Arg Leu Arg 310					
gcg agt cag ttc Ala Ser Gln Phe	• •				-
gcg acc ctc cac Ala Thr Leu His 345					_
gat cac gaa atc Asp His Glu Ile 360	•	_		_	-
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Leu Gln Leu Glu 35	Asn Gly Ile	Ile Thr Glu 40	Leu Ser Gly 45	Glu Pro	Ala
Pro Lys Asn Ala 50	Gly Phe His 55	Pro Glu Leu	Pro Thr Ile 60	Val Pro	Ser

Phe 65	Ile	Asp	Leu	His	Asn 70	His	Gly	Gly	Asn	Gly 75	Gly	Ala	Phe	Pro	Thr 80
Gly	Thr	Gln	Asp	Gln 85	Ala	Arg	Asn	Ala	Ala 90	Gln	Tyr	His	Arg	Glu 95	His
Gly	Thr	Thr	Val 100	Met	Leu	Ala	Ser	Met 105	Val	Ser	Ala	Pro	Ala 110	Asp	Ala
Leu	Ala	Ala 115	Gln	Val	Glu	Asn	Leu 120	Ile	Pro	Leu	Cys	Glu 125	Glu	Gly	Leu
Leu	Cys 130	Gly	Ile	His	Leu	Glu 135	Gly	Pro	Phe	Ile	Asn 140	Ala	Cys	Arg	Cys
Gly 145	Ala	Gln	Asn	Pro	Asp 150	Phe	Ile	Phe	Pro	Gly 155	Asn	Pro	Thr	Asp	Leu 160
Ala	Gln	Val	Ile	His 165	Ala	Gly	Lys	Gly	Trp 170	Ile	Lys	Ser	Ile	Thr 175	Val
Ala	Pro	Glu	Thr 180	Asp	Asn	Leu	Thr	Glu 185	Leu	Leu	Asp	Leu	Cys 190	Ala	Ala
His	His	Ile 195	Ile	Ala	Ser	Phe	Gly 200	His	Thr	Asp	Ala	Asp 205	Phe	Asp	Thr
Thr	Thr 210	Ser	Ala	Ile	Ala	Leu 215	Ala	Lys	Glu	Lys	Asn 220	Val	Thr	Val	Thr
Ala 225	Thr	His	Leu	Phe	Asn 230	Ala	Met	Pro	Pro	Leu 235	His	His	Arg	Asp	Pro 240
Gly	Ser	Val	Gly	Ala 245	Leu	Leu	Ala	Ala	Ala 250	Arg	Ala	Gly	Asp	Ala 255	Tyr
Val	Glu	Leu	Ile 260	Ala	Asp	Gly	Val	His 265	Leu	Ala	Asp	Gly	Thr 270	Val	Asp
Leu	Ala	Arg 275	Ser	Asn	Asn	Ala	Phe 280	Phe	Ile	Thr	Asp	Ala 285	Met	Glu	Ala
Ala	Gly 290	Met	Pro	Asp	Gly	Glu 295	Tyr	Ile	Leu	Gly	Val 300	Leu	Asn	Val	Thr
Val 305	Thr	Asp	Gly	Val	Ala 310	Arg	Leu	Arg	Asp	Gly 315	Gly	Ala	Ile	Ala	Gly 320
Gly	Thr	Ser	Thr	Leu 325	Ala	Ser	Gln	Phe	Val 330	His	His	Val	Arg	Arg 335	Gly
Met	Thr	Leu	11e 340	Asp	Ala	Thr	Leu	His 345	Thr	Ser	Thr	Val	Ala 350	Ala	Lys
Ile	Leu	Gly 355	Leu	Ser	Asp	His	Glu 360	Ile	Val	Lys	Ser	Asn 365	Pro	Val	Asn
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385

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Ala	Gly	Lys	Gly	Trp 170	Ile	Lys	Ser	Ile	Thr 175	Val	Ala	Pro	Glu	Thr 180	Asp	
											cac His					691
					-	_	_		-		act Thr		-	-		739
											gct Ala 225					787
											ggc Gly					835
_		-		-	_	-		_	•		gtt Val		_		_	883
											cta Leu					931
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	-			_		_	_		-		gtc Val 305		_		_	1027
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	_	_						-			atg Met	_			_	1123
							_	_	-		att Ile					1171
_		-		-					_		ttt Phe		_		_	1219
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<213> Corynebacterium glutamicum

<400> 416

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Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe $20 \hspace{1cm} 25 \hspace{1cm} 30$

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala 35 40 45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr 65 70 75 80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
85 90 95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala 100 105 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu 115 120 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys 130 135 140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu 145 150 155 160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val 165 170 175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala 180 185 190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr 195 200 205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr 210 215 220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro 225 230 235 240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr 245 250 255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp 260 265 270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala 275 280 285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr 290 295 300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly

305 310 315 320 Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly 330 325 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile 385 <210> 417 <211> 1584 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1561) <223> RXN01752 <400> 417 gaaatgacgt gaccatcgat accaataccc aattgaaaga tcttgacctg gtcagccaag 60 ttggccgtca gatcgtggca gaacaacagg tggggaggtc atg atg gaa caa gat Met Met Glu Gln Asp ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163 Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys 10 211 aag get gea etg att gat gee att gaa ggg tta agg gtg ege gat eeg Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc 259 Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe att gct gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa 307 Ile Ala Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln 355 qca qca ctt att qqa ctg tca qca acg tgt acg ttc atg tac ctc att Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403 Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu 95 451 tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp

105 110 115

aag Lys	ctg Leu	aaa Lys 120	acc Thr	tac Tyr	acg Thr	gtg Val	ttg Leu 125	gtg Val	ccc Pro	gcc Ala	tat Tyr	ggc Gly 130	gaa Glu	cct Pro	gag Glu	499
					ctg Leu											547
cat His 150	ctt Leu	ctg Leu	cag Gln	gta Val	ttg Leu 155	ctc Leu	atg Met	ttg Leu	gag Glu	gaa Glu 160	gat Asp	gat Asp	ctg Leu	ccc Pro	acg Thr 165	595
atc Ile	gcc Ala	gcg Ala	gca Ala	gag Glu 170	gca Ala	gcg Ala	gga Gly	gtg Val	gat Asp 175	cag Gln	gtg Val	gca Ala	acg Thr	atc Ile 180	att Ile	643
aag Lys	gtg Val	ccg Pro	cca Pro 185	gcg Ala	cag Gln	ccc Pro	cgc Arg	acc Thr 190	aag Lys	ccg Pro	aag Lys	gcc Ala	tgt Cys 195	aac Asn	tat Tyr	691
gga Gly	ttg Leu	cac His 200	ttt Phe	gcc Ala	acg Thr	ggg Gly	gaa Glu 205	att Ile	gtc Val	acg Thr	atc Ile	ttt Phe 210	gac Asp	gcg Ala	gaa Glu	739
					ctc Leu											787
					acg Thr 235											835
					ctg Leu											883
					ctg Leu											931
gtc Val	cca Pro	ttg Leu 280	ggc Gly	ggt Gly	acc Thr	tcc Ser	aac Asn 285	cat His	ctg Leu	ctc Leu	acg Thr	ggt Gly 290	gtc Val	ctg Leu	aaa Lys	979
					gat Asp											1027
ggc Gly 310	gta Val	ccc Pro	atc Ile	gcg Ala	gca Ala 315	aaa Lys	gga Gly	tat Tyr	tcc Ser	acc Thr 320	gcg Ala	gtg Val	ttg Leu	gat Asp	tcg Ser 325	1075
					gca Ala											1123
					aag Lys											1171

					tta Leu											1219
					atg Met											1267
					ttg Leu 395											1315
					ttc Phe											1363
					aat Asn											1411
tgc Cys	cgg Arg	gaa Glu 440	ggc Gly	cgc Arg	gac Asp	ccc Pro	ttg Leu 445	ctg Leu	ctc Leu	atc Ile	gcg Ala	gtt Val 450	ctc Leu	acg Thr	ttc Phe	1459
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<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly 35 40 45

Gln Lys Val Ala Phe Ile Ala Val Val Gly Phe Ile Leu Met Leu 50 55 60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr 65 70 75 80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala 120 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr Ile Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr 200 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val 215 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser 230 235 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met 260 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr 345 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile 375 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr 405 410

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe 425 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala 485 <210> 419 <211> 689 <212> DNA <213> Corynebacterium glutamicum <221> CDS <222> (19)..(666) <223> FRXA01839 <400> 419 ttcctgctgc caggtgtcatg cgc atg aac gca cct gtc cca ttg ggc ggt 51 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly 99 ace tee aac cat etg ete aeg ggt gte etg aaa gat ete gge geg tgg Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp 147 gat ect tte aat gte aca gaa gat geg gae ete gge gta ege ate geg Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala gca aag gga tat too aco gog gtg ttg gat tog gtg acg tgg gag gaa 195 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu 50 gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr 291 aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu 387 atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr 115 435 ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met

125 130 135 ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc 483 Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc 531 Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg gac ecc ttg etg etc ate geg gtt etc acg tte eeg etg tat tgg etg 579 Asp Pro Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu 175 ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga 627 Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg 190 cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcggtgc 676 Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala 689 ccatcgtcaa acc <210> 420 <211> 216 <212> PRT <213> Corynebacterium glutamicum Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu 10 Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser 35 Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile 150 155

Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala <210> 421 <211> 1050 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1027) <223> RXA01859 <400> 421 tacgcccagg gtttccatat tggtaaatct aagccgattg atgaatttat agctacttat 60 ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc 115 Met Lys Lys Ser 1 ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg 163 Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly 10 atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca 211 Met Gly Ile Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala 35 tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc 259 Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu 40 ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc 307 Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile 55 gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta 355 Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val 70 75 acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg 403 Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala 100 451 ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile 105 115 499 acc att aac gtg ctc gtg cca gca cac aat gag gcg gaa aga att act Thr Ile Asn Val Leu Val Pro Ala His Asn Glu Ala Glu Arg Ile Thr 120 125

gga aca att Gly Thr Ile 135	cag gca ttg Gln Ala Leu	aaa tca caa Lys Ser Gln 140	cat gag cct His Glu Pro 145	cca gaa cgc atc Pro Glu Arg Ile	547
gtt gta gtt Val Val Val 150	gcc gat aat Ala Asp Asn 155	Cys Thr Asp	gaa act acg Glu Thr Thr 160	gaa tta gcc cgt Glu Leu Ala Arg 165	595
gct gag gga Ala Glu Gly	gtg gag gtc Val Glu Val 170	ttg gaa aca Leu Glu Thr	gtc aat aat Val Asn Asn 175	aag ttt aag aag Lys Phe Lys Lys 180	643
Ala Gly Gly	ctc aat cag Leu Asn Gln 185	gct ttg agc Ala Leu Ser 190	cgg atg ctt Arg Met Leu	ccc aca ttg ggg Pro Thr Leu Gly 195	691
				gca ctt gat caa Ala Leu Asp Gln 210	739
				gat cgc gct cta Asp Arg Ala Leu	787
				tcc gga tgg ctt Ser Gly Trp Leu 245	835
				cgt gac atc tat Arg Asp Ile Tyr 260	883
Arg Arg Arg				gcg tcg gct ttt Ala Ser Ala Phe 275	931
				ggg aca ttg atc Gly Thr Leu Ile 290	979
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Leu Ser Asp	Pro Ala Ser	Pro Gly Ala	Lys Glu Thr	Glu Val Phe Asp	

35 40 45

Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu 50 55 60

Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr
65 70 75 80

Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu 85 90 95

Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val 100 105 110

Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu 115 120 125

Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu 130 135 140

Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr 145 150 155 160

Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn 165 170 175

Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met 180 185 190

Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp 195 200 205

Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu 210 215 220

Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser 225 230 235 240

Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr
245 250 255

Ser Arg Asp Ile Tyr Arg Arg Gly Arg Val Phe Val Leu Thr Gly 260 265 270

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Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala 290 295 300

Gly Val Asp Arg Arg 305

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<211> 882

<212> DNA

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<220>

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787

835

882

atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile 220 gtt gat gaa gca gca tcc aag ctg gaa aac gct gat cac tac cgt Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg 235 240 ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg Leu Met Glu Gln Leu Lys Leu Arg 250 <210> 424 <211> 253 <212> PRT <213> Corynebacterium glutamicum Met Asp Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala 10 Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu 20 Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser 135 Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu 145 Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala 170 Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu 200 Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn 210 215

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					acc Thr 155											595
					ctg Leu											643
					cgt Arg											691
					gga Gly											739
cgc Arg	aag Lys 215	gct Ala	gta Val	gag Glu	ctg Leu	gct Ala 220	aat Asn	gac Asp	cag Gln	gtt Val	gtt Val 225	acc Thr	atc Ile	acc Thr	gct Ala	787
					acc Thr 235											835
cct Pro	ttc Phe	gac Asp	gtg Val	gag Glu 250	tgg Trp	gac Asp	gct Ala	gca Ala	gct Ala 255	gct Ala	gaa Glu	aag Lys	ggt Gly	ggc Gly 260	ttc Phe	883
					aag Lys											931
					cgt Arg										gat . Asp	979
					gaa Glu											1027
					act Thr 315											1075
					tgc Cys											1123
					gac Asp											1171
					ggc Gly											1219
cac His	gca Ala 375	cgt Arg	gag Glu	cag Gln	ggt Gly	gcc Ala 380	aag Lys	gtt Val	gtt Val	gct Ala	att Ile 385	tgt Cys	aac Asn	act Thr	gtt Val	1267
gga	tcc	act	ctt	сса	cgt	gaa	gca	gat	gcg	tcc	ctg	tac	acc	tac	gct	1315

Gly Ser Thr Leu Pro Arg Glu Ala Asp 390 395	Ala Ser Leu Tyr Thr Tyr Ala 400 405	
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act gct tct tac ttg ctt ggc ctg tac Thr Ala Ser Tyr Leu Leu Gly Leu Tyr 425 430	ttg gct cag ctg cgc ggc aac 14 Leu Ala Gln Leu Arg Gly Asn 435	11
aag ttc gct gat gag gtt tct tcc att Lys Phe Ala Asp Glu Val Ser Ser Ile 440 445	ctg gac agc ctg cgt gag atg 14 Leu Asp Ser Leu Arg Glu Met 450	59
cct gag aag att cag cag gtc atc gat Pro Glu Lys Ile Gln Gln Val Ile Asp 455 460		07
ctt ggc caa gat atg gca gat gct aag Leu Gly Gln Asp Met Ala Asp Ala Lys 470 475		55
cac gtt ggt ttc cca gtt gcg ctt gag His Val Gly Phe Pro Val Ala Leu Glu 490		03
atc gca tac ctg cac gct gaa ggt ttc Ile Ala Tyr Leu His Ala Glu Gly Phe 505 510	gct gca ggc gag ctc aag cac 16 Ala Ala Gly Glu Leu Lys His 515	51
ggc cca att gct ttg gtt gag gaa ggc Gly Pro Ile Ala Leu Val Glu Glu Gly 520 525	cag ccg atc ttc gtt atc gtg 16 Gln Pro Ile Phe Val Ile Val 530	99
cct tca cct cgt ggt cgc gat tcc ctg Pro Ser Pro Arg Gly Arg Asp Ser Leu 535 540		47
att cag gag atc cgt gca cgt ggc gct Ile Gln Glu Ile Arg Ala Arg Gly Ala 550 555		95
gaa ggc gat gag gct gtc aac gat tac Glu Gly Asp Glu Ala Val Asn Asp Tyr 570	gcc aac ttc atc atc cgc att 18 Ala Asn Phe Ile Ile Arg Ile 575 580	43
cct cag gcc cca acc ctg atg cag cct Pro Gln Ala Pro Thr Leu Met Gln Pro 585 590	* *	91
cag atc ttt gcg tgc gct gtg gca acc Gln Ile Phe Ala Cys Ala Val Ala Thr 600 605		39
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<211> 625

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

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Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly
35 40 45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala 50 55 60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His 65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro 85 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile 100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn 115 120 125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu 130 135 140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu 145 150 155 160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala 165 170 175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val 180 185 190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly
195 200 205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val 210 215 220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser 225 230 235 240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala 245 250 255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln 260 265 270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly 275 280 285

Lys	Leu 290	Val	Leu	Asp	Glu	Leu 295	Arg	Ile	Asp	Glu	Ala 300	Ile	Leu	Arg	Ser
Val 305	Asp	Lys	Ile	Val	Ile 310	Val	Ala	Cys	Gly	Thr 315	Ala	Ala	Tyr	Ala	Gly 320
Gln	Val	Ala	Arg	Tyr 325	Ala	Ile	Glu	His	Trp 330	Cys	Arg	Ile	Pro	Thr 335	Glu
Val	Glu	Leu	Ala 340	His	Glu	Phe	Arg	Tyr 345	Arg	Asp	Pro	Ile	Leu 350	Asn	Glu
Lys	Thr	Leu 355	Val	Val	Ala	Leu	Ser 360	Gln	Ser	Gly	Glu	Thr 365	Met	Asp	Thr
Leu	Met 370	Ala	Val	Arg	His	Ala 375	Arg	Glu	Gln	Gly	Ala 380	Lys	Val	Val	Ala
Ile 385	Cys	Asn	Thr	Val	Gly 390	Ser	Thr	Leu	Pro	Arg 395	Glu	Ala	Asp	Ala	Ser 400
Leu	Tyr	Thr	Tyr	Ala 405	Gly	Pro	Glu	Ile	Ala 410	Val	Ala	Ser	Thr	Lys 415	Ala
Phe	Leu	Ala	Gln 420	Ile	Thr	Ala	Ser	Tyr 425	Leu	Leu	Gly	Leu	Tyr 430	Leu	Ala
Gln	Leu	Arg 435	Gly	Asn	Lys	Phe	Ala 440	Asp	Glu	Val	Ser	Ser 445	Ile	Leu	Asp
Ser	Leu 450	Arg	Glu	Met	Pro	Glu 455	Lys	Ile	Gln	Gln	Val 460	Ile	Asp	Ala	Glu
Glu 465	Gln	Ile	Lys	Lys	Leu 470	Gly	Gln	Asp	Met	Ala 475	Asp	Ala	Lys	Ser	Val 480
Leu	Phe	Leu	Gly	Arg 485	His	Val	Gly	Phe	Pro 490	Val	Ala	Leu	Glu	Gly 495	Ala
Leu	Lys	Leu	Lys 500	Glu	Ile	Ala	Tyr	Leu 505	His	Ala	Glu	Gly	Phe 510	Ala	Ala
Gly	Glu	Leu 515	Lys	His	Gly	Pro	Ile 520	Ala	Leu	Val	Glu	Glu 525	Gly	Gln	Pro
Ile	Phe 530	Val	Ile	Val	Pro	Ser 535	Pro	Arg	Gly	Arg	Asp 540	Ser	Leu	His	Ser
Lys 545	Val	Val	Ser	Asn	Ile 550	Gln	Glu	Ile	Arg	Ala 555	Arg	Gly	Ala	Val	Thr 560
Ile	Val	Ile	Ala	Glu 565	Glu	Gly	Asp	Glu	Ala 570	Val	Asn	Asp	Tyr	Ala 575	Asn
Phe	Ile	Ile	Arg 580	Ile	Pro	Gln	Ala	Pro 585	Thr	Leu	Met	Gln	Pro 590	Leu	Leu
Ser	Thr	Val 595	Pro	Leu	Gln	Ile	Phe 600	Ala	Cys	Ala	Val	Ala 605	Thr	Ala	Lys
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PCT/IB00/00943 WO 01/00844

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144

192

240

288

336

384

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618

576

624

666

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Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala 180 185 190

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	gcc Ala															240
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Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp

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125

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125

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75

65 70

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215 220 . 225

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979 gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp 285 1027 gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn 300 1065 gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt Val Ala Asp Phe Lys <210> 440 <211> 314 <212> PRT <213> Corynebacterium glutamicum <400> 440 Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val 85 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Pro Ser Val Glu 100 105 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser 120 125 115 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly 135 Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly 145 150 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser 180 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe 215 220

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Arg	Ala	Gly	Glu	Asp 245	Val	Ile	Val	Val	Gly 250	Phe	Asp	Gly	Thr	Asn 255	Asp	
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Gln	Pro	Glu 275	Glu	Leu	Gly	Ala	Lys 280	Ala	Val	Glu	Glu	Ala 285	Ala	Lys	Leu	
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ctg cag gca Leu Gln Ala	aaa ctt g Lys Leu A 170	ct caa ga la Gln As	c cgc agc p Arg Ser 175	att gat t Ile Asp T	gg gtt gtg rp Val Val 180	gga 643 Gly
ctc cag gct Leu Gln Ala						
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acc gct att Thr Ala Ile 215						
tat ctg cag Tyr Leu Gln 230	Gly Tyr M					
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Ser Ser Asn Pro Glu Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala 35 40 45

Ile Asp Ser Arg Val Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln
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Ser Leu Gly Pro Val Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val 65 70 75 80

Val Gly Leu Asn Ala Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr 85 90 95

Gly Phe Phe Gly Gln Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala 100 105 110

Arg Leu Ala Glu Glu Asn Ala Gln Lys Val Leu Cys Val Ile His Glu 115 120 125

Gln Gly Asn Ser Ser Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly 130 135 140

Leu Gly Lys Gln Val Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr 145 150 155 160

Ser Val Asn Ser Thr Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile 165 170 175

Asp Trp Val Val Gly Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp 180 185 190

Ala Ala Asp Ala Ala Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr 195 200 205

Asn Ala Gln Leu Met Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala 210 215 220

Ile Asp Gln Gln Pro Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu 225 230 235 240

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caa ctc acc tcc Gln Leu Thr Ser	cac acc acc His Thr Thr 10	gac atc gaa ggc Asp Ile Glu Gly 15	cta ctg gtt Leu Leu Val	ttc gat 163 Phe Asp 20
	Gly Asp Asn	cgc ggc tgg ttc Arg Gly Trp Phe 30		
cgc acc aag ato Arg Thr Lys Met 40	acc aac ctg Thr Asn Leu	ggg ctg ccc gat Gly Leu Pro Asp 45	ttt ggc ccc Phe Gly Pro 50	gtc caa 259 Val Gln
aac aac atg agt Asn Asn Met Sei 55	ttc aac gcc Phe Asn Ala 60	acc gcc ggc acg Thr Ala Gly Thr	act cgc ggc Thr Arg Gly 65	atg cac 307 Met His
gct gag ccg tgg Ala Glu Pro Trp 70	gat aaa ttt Asp Lys Phe 75	gtg tcc gtc gcg Val Ser Val Ala 80	Val Gly Ser	gtt ttc 355 Val Phe 85
gga gct tgg gto Gly Ala Trp Val	gat ctg cgc Asp Leu Arg 90	gcg ggc tcg agc Ala Gly Ser Ser 95	acg tac ggt Thr Tyr Gly	aac gtc 403 Asn Val 100
	: Ile Thr Pro	gac gtg gga gtt Asp Val Gly Val 110		
gtg gca aac ggg Val Ala Asn Gly 120	ttc cag gcg Phe Gln Ala	ctc gag gac ggc Leu Glu Asp Gly 125	acg ctg tac Thr Leu Tyr 130	acc tac 499 Thr Tyr
		ccc gac gcg cat Pro Asp Ala His		
	Asp Trp Pro	ctg ccc atc acc Leu Pro Ile Thr 160	Glu Ile Ser	
		atc gac gcc acc Ile Asp Ala Thr 175		
aag gtt ctc gto Lys Val Leu Val 189	. Val Gly Ala	ggc gga caa ctg Gly Gly Gln Leu 190	gga acc gcg Gly Thr Ala 195	cta cgc 691 Leu Arg
		ttt gtc acg cgc Phe Val Thr Arg 205		
acc tca gat cto Thr Ser Asp Leo 215	c acc gag gct Thr Glu Ala 220	cgc gcg tgg aaa Arg Ala Trp Lys	caa tac tcc Gln Tyr Ser 225	acc atc 787 Thr Ile

ata aac gcc gcc gcc tac act gcc gtt gac of the Asn Ala Ala Ala Tyr Thr Ala Val Asp (230)	cag gca gaa cac gac cgc 839 Gln Ala Glu His Asp Arg 240 245	5
gca gca gcg tgg gac atc aac gca gcg gca c Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala 250 255	gtg gct aac ctc gcg acc 883 Val Ala Asn Leu Ala Thr 260	3
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cca ctc ggc gtg tac ggc caa tcc aaa gca c Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala 2 295 300	gcc ggc gac atc gga gac 102 Ala Gly Asp Ile Gly Asp 305	27
acc acc gca ccg cgc cac tac att gtg cgc of the Thr Ala Pro Arg His Tyr Ile Val Arg 1310	acc agc tgg gtg att ggc 10° Thr Ser Trp Val Ile Gly 325	75
gat ggc aat aat ttt gtc cgc acc atg aaa Asp Gly Asn Asn Phe Val Arg Thr Met Lys 330	tcc ctc gac gaa cgc ggc 113 Ser Leu Asp Glu Arg Gly 340	23
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gaa gac atc gca gcc ggc atc gcg cac ctt Glu Asp Ile Ala Ala Gly Ile Ala His Leu 360 365		19
tat ggc acc tac aac ctc acc aac acc ggc of Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly 375		67
gat gtt gcc cgc gca gta ttt tcc gac ccc Asp Val Ala Arg Ala Val Phe Ser Asp Pro 390	acc aaa gtt acc ggc gtg 13: Thr Lys Val Thr Gly Val 400 405	15
age ace gee gag tae tte gee aac aaa gae s Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp 410	gca gcg ccc cgc cca ctg 13 Ala Ala Pro Arg Pro Leu 420	63 [°]
aac tcc gtt ttg gat ctc ggc aaa atc gaa Asn Ser Val Leu Asp Leu Gly Lys Ile Glu 425 430	gcc acc gga ttt agc gca 14: Ala Thr Gly Phe Ser Ala 435	11
ccg acc tgg cag acc cgc ctc aac gac tac Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr 440 445	ctc aag gaa ctc tca aag 149 Leu Lys Glu Leu Ser Lys 450	59
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Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr 145 150 155 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr 165 170 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu 180 185 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg 195 200 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys 210 215 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln 225 230 235 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Val 245 250 255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
260 265 270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu 275 280 285

Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala 290 295 300

Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr 310 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr 390 395 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala 410 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala 425 430 420 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu 440 435 Lys Glu Leu Ser Lys 450 <210> 445 <211> 449 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(426) <223> FRXA01569 <400> 445 48 gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc gat ggc Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala 20 cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp 35 ate gea gee gge ate geg cae ett ttg gaa gtg ggt gea gea tat gge 192 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly 50 ace tac aac etc ace aac ace gge gaa eee gea age tgg gee gat gtt 240 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val 65

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gcc gag tac tto Ala Glu Tyr Pho 100	Ala Asn										336
gtt ttg gat cto Val Leu Asp Leu 115		-	Āla				_	-	_		384
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Pro Ser Val Va	Asp Asp	Gln Ile 40		Arg	Leu	Ser	Phe 45	Thr	Glu	Asp	
Ile Ala Ala Gl	/ Ile Ala	His Leu 55	Leu	Glu	Val	Gly 60	Ala	Ala	Tyr	Gly	
Thr Tyr Asn Let	Thr Asn 70		Glu	Pro	Ala 75	Ser	Trp	Ala	Asp	Val 80	
Ala Arg Ala Va	Phe Ser 85	Asp Pro	Thr	Lys 90	Val	Thr	Gly	Val	Ser 95	Thr	
Ala Glu Tyr Pho		Lys Asp	Ala 105	Ala	Pro	Arg	Pro	Leu 110	Asn	Ser	
Val Leu Asp Le 115	Gly Lys	Ile Glu 120		Thr	Gly	Phe	Ser 125	Ala	Pro	Thr	
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acc tca gat Thr Ser Asp 215	ctc acc Leu Thr	gag gc Glu Al 22	a Arg	gcg Ala	tgg Trp	aaa Lys	caa Gln 225	tac Tyr	tcc Ser	acc Thr	atc Ile	787
ata aac gcc Ile Asn Ala 230												835
gca gca gcg Ala Ala Ala		Ile As										883
tcg cgc gcg Ser Arg Ala												931
tct tcg acg Ser Ser Thr 280	gtg cgg Val Arg	gcg aa Ala As	t cct n Pro 285	acg Thr	atg Met	aaa Lys	acg Thr	cac His 290	cgt Arg	ttt Phe	ccc Pro	979
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Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His 130 135135140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr 150 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr 170 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg 200 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys 280 Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro 295 Ala Thr Ser 305 . <210> 449 <211> 1056 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1033) <223> RXA00825 <400> 449 cocqttcatq ctqqqctttq qtqcqqtqat qqcaactatt tqtctqatca ttqtqaqttt 60 tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt Met Arg Thr Val Val ace ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211 Lys Glu Gly His Glu Val Val Ile Asp Asn Leu Ser Arg Gly Arg 259 ctg gag aat etc tee gat geg gaa gee ace gga aaa etc ace ttt gtg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val

40 45 50

					gac Asp								307
					ttc Phe 75								355
					ctt Leu								403
	_		-	_	gct Ala	_	_	_					451
					ggt Gly								499
					cca Pro								547
					att Ile 155								595
					atc Ile								643
					gca Ala								691
					acc Thr								739
_		-		-	ggt Gly	_	_	-	_	-		-	787
					gga Gly 235								835
					ctg Leu								883
					tat Tyr								931
					ggc Gly								979

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Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val 280 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr 295 Val Glu Tyr Phe Arg Thr His <210> 451 <211> 1140 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1117) <223> RXA02054 <400> 451 cctaatgaac agccggagca ccctggtcgt ttgcagaata ggcgcatcga caacagctac 60 taactctgcc agctcgcccg gacgaactaa ggtagacggc atg act tct ttg ctt Met Thr Ser Leu Leu 163 gtq acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr 10 gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc 211 Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc 307 Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser 355 ctq gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His aac gac aac too oto aac gac ooc too cog ttt gtt cac act aac oto 403 Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu 95 451 atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg 105 110

ttc Phe					acc Thr											499
gat Asp	cca Pro 135	aac Asn	cgc Arg	ttc Phe	act Thr	gaa Glu 140	acc Thr	acc Thr	gcc Ala	tac Tyr	aag Lys 145	cca Pro	tcg Ser	tct Ser	cca Pro	547
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att Ile	ctg Leu	gcc Ala 200	ggc Gly	ctg Leu	aca Thr	cca Pro	aaa Lys 205	ctt Leu	tat Tyr	gga Gly	acc Thr	ggc Gly 210	gag Glu	cag Gln	gtc Val	739
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					atc Ile 235											835
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Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
50 60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe 65 70 75 80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe 85 90 95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg 100 105 110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
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Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr 130 135 140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu 145 150 155 160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn 165 170 175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro 180 185 190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly 195 200 205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp 210 215 220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile 225 230 235 240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu 245 250 255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala 260 265 270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu 275 280 285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly 290 295 300

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135 140 145 cqc qqc qat qag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg 595 Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu 155 ccq ttt qqt acq tqt ttq acc acq qcg tat ttg cac ccg gat ggt tct 643 Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg 691 Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro 185 739 gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu 205 200 atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc 787 Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg 215 220 ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg 235 240 883 qag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg 250 255 909 ccc tagatcagtt ttagtagttc ctc Pro

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Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu 50 60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser 65 70 75 80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu 85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro 100 105 110

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Tyr 145	Arg	Leu	Phe	Ile	Arg 150	Gly	Asp	Glu	Val	Glu 155	Tyr	His	Arg	Arg	Leu 160	
Val	Arg	Ser	Gly	Leu 165	Pro	Phe	Gly	Thr	Cys 170	Leu	Thr	Thr	Ala	Tyr 175	Leu	
His	Pro	Asp	Gly 180	Ser	Asp	Glu	Phe	Lys 185	Pro	Ile	Leu	Gly	Gly 190	Arg	Met	
His	Thr	Gln 195	Tyr	Pro	Asp	Asn	Asp 200	Phe	Lys	Arg	Phe	Phe 205	Thr	Tyr	Arg	
Asn	Arg 210	Gly	Tyr	Leu	Met	Ser 215	Gln	Pro	Gly	Met	Arg 220	Lys	Leu	Leu	Pro	
Gln 225	Glu	Tyr	Ala	Arg	Phe 230	Ala	Trp	Phe	Phe	Leu 235	Val	Gln	Lys	Arg	Asp 240	
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		gtg Val														211
		cgc Arg 40														259

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ctg Leu 70	ggt Gly	Gly	cgg Arg	atg Met	cat His 75	acg Thr	cag Gln	tat Tyr	ccg Pro	gat Asp 80	aat Asn	gat Asp	ttc Phe	aag Lys	agg Arg 85	355
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gtt Val	cag Gln	aaa Lys 120	cgg Arg	gat Asp	gtg Val	aag Lys	gga Gly 125	ttc Phe	cgg Arg	gag Glu	tgg Trp	ctg Leu 130	cgc Arg	ctg Leu	cac His	499
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                                                                   115
                                            Met Ile Gln Ala Ala
ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg
                                                                   163
Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu
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Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val
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Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys Leu Asp Arg Arg Val
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Met Val Ala Gly Thr Gly Met Ala Asn Met Ser Ala Tyr Ile Cys Ala
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                         60
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Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu Asp Trp Asn Ala Asp
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 70
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Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val Ala Trp Leu Gly Leu
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                                                         100
                 90
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Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu Ala Val Cys Leu Leu
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            105
ctg cag cgt cga aaa aat att gct ttt cga cgc taaaacccga ccgtaaccgc 504
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653

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tat at Tyr Me																451
tct go Ser Al	la F															499
tct to Ser Tr	gg a rp T 35	aca Thr	cct Pro	gtg Val	ttg Leu	cag Gln 140	cag Gln	ctc Leu	acg Thr	ggc Gly	gct Ala 145	ttt Phe	ggc Gly	ttt Phe	gtg Val	547
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Val G. 1 Leu Th Phe G. Ser A: Ala G. 65	ly V ly V rg I 50 ln I	Val Ala Val 35 Leu Ile	Met 20 Ala Ala Pro	5 Cys Gly Val Met	Val Val Phe Gly 70	Tyr His Thr 55 Met	Ile Ala 40 Ser Leu Ile	Val 25 Ile Val Val	Ala Asp Gln Asp Ala 90	Ile Arg Val Arg 75 Ala	Ala Phe Gly 60 Phe	Gly Asp 45 Val Asp Gln	Arg 30 Ile Tyr Ala Leu	15 Thr Asp Val Arg Ile 95	Ser Ala Leu Lys 80 Leu	
Val G. 1 Leu Ti Phe G. Ser A. 4 Ala G. 65 Leu Le	ly V ly V rg I 50 ln I eu I	Val Ala Val 35 Leu Ile	Met 20 Ala Ala Pro Ala Asp 100	5 Cys Gly Val Met Gly 85 Ser	Val Val Phe Gly 70 Ala	Tyr His Thr 55 Met Leu Met	Ile Ala 40 Ser Leu Ile	Val 25 Ile Val Val Leu Ala 105	Ala Asp Gln Asp Ala 90 Ile	Ile Arg Val Arg 75 Ala	Ala Phe Gly 60 Phe Gly Ala	Gly Asp 45 Val Asp Gln Arg	Arg 30 Ile Tyr Ala Leu Val 110	15 Thr Asp Val Arg Ile 95 Leu	Ser Ala Leu Lys 80 Leu Ile	
Val G. Leu Ti Phe G. Ser A. Ala G. 65 Leu Le Gly Pi Ser Va Asn Ti	ly V hr A ly V rg I 50 ln I eu I	Val Ala Val 35 Leu Ile Leu Thr	Met 20 Ala Ala Pro Ala Asp 100 Asp	5 Cys Gly Val Met Gly 85 Ser	Val Val Phe Gly 70 Ala Tyr	Tyr His Thr 55 Met Leu Met	Ile Ala 40 Ser Leu Ile Ile Phe 120	Val 25 Ile Val Val Leu Ala 105 Leu	Ala Asp Gln Asp Ala 90 Ile Ser	Ile Arg Val Arg 75 Ala Phe	Ala Phe Gly 60 Phe Gly Ala	Gly Asp 45 Val Asp Gln Arg Arg 125	Arg 30 Ile Tyr Ala Leu Val 110 Leu	15 Thr Asp Val Arg Ile 95 Leu Leu	Ser Ala Leu Lys 80 Leu Ile	

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Tyr Ser Thr Pro

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gaa Glu	gca Ala	gat Asp	aaa Lys 185	cca Pro	agc Ser	ctg Leu	cgc Arg	gcg Ala 190	agt Ser	ttg Leu	aag Lys	ttg Leu	att Ile 195	gtc Val	cgc Arg	691
aat Asn	ccg Pro	att Ile 200	acg Thr	tgg Trp	cag Gln	ggt Gly	ttc Phe 205	ttc Phe	att Ile	cac His	tac Tyr	gta Val 210	ttg Leu	atg Met	gtg Val	739
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						acg Thr										835
						tcg Ser										883
_				_	_	gac Asp		-	_			_	_		_	931
		-	-		-	gtg Val		-	-		_	_		-		979
						gtc Val 300										1027
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						tgg Trp										1219
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Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile

265

260

270

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					act Thr											403
					aac Asn											451
					cca Pro											499
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					ggt Gly 155											595
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					ctg Leu											691
					aac Asn											739
					gca Ala											787
					acc Thr 235											835
					gat Asp											883
					cat His											931
					atc Ile											979
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gat ttc Asp Phe 310	cca gtc Pro Val	cgg tcc Arg Ser 315	atg gt Met Va	tg att al Ile	gac Asp	cgc Arg 320	atc Ile	gag Glu	gtc Val	acc Thr	gga Gly 325	1075
tct ccc Ser Pro	gca gta Ala Val	tct gaa Ser Glu 330	gac ao Asp Tl	cc ccc hr Pro	atg Met 335	cca Pro	gat Asp	acc Thr	acc Thr	cag Gln 340	ctt Leu	1123
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		gaa ccg Glu Pro										1411
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		tac tcg Tyr Ser										1651
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Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg	

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Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys 200

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys

Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr 230 235

Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg 250

Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp 265

Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp 275

Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro

Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg

Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro

Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg

Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp

Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln 375 - 380

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Ile	Ala	Thr	Pro 420	Glu	Asn	Ala	Gln	Glu 425	Glu	Pro	Cys	Ala	Pro 430	Gly	Glu
Val	Thr	Arg 435	Tyr	Ser	Ser	Ala	Arg 440	Val	His	Leu	Pro	Glu 445	Ile	Pro	Ala
Gly	Asn 450	Phe	Arg	Leu	Thr	Val 455	Arg	Ala	Arg	Ala	Gln 460	Ser	Glu	Glu	Leu
Val 465	Asp	Gly	Val	Arg	Pro 470	Ala	Ile	Trp	Met	Gln 475	Asn	Asn	Thr	Asn	Phe 480
Cys	Ala	Asp	Asn	Asp 485	Gly	Arg	Pro	Tyr	Gly 490	Glu	Leu	Asp	Ile	Thr 495	Glu
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Cys	Ala	Gly 51,5	Asn	Arg	Pro	Glu	Met 520	Lys	Leu	Arg	Gln	Met 525	Glu	Met	Glu
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Lys	Asp	Val	Phe	Gly 565	Asn	Ser	Val	Thr	Pro 570	Ala	Ala	Ala	Pro	Leu 575	Arg
Pro	Ala	His	Phe 580	Lys	Leu	Ser	Glu	Glu 585	Glu	Tyr	Arg	Glu	Val 590	Ile	Gly
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Arg 625	Phe	Gln	Ile	Asp	His 630	Val	Ala	Val	Asp	11e 635	Glu	Ser	Asp	Ser	Val 640
Asp	Asn	Val	Trp	Pro 645	Asp	Ala	Ala	Asn	Glu 650	Ile	Pro	Asp	Asn	Val 655	Gly
Ile	Glu	Asp	Ser 660	Asp	Asp	Gly	Ser	Asp 665	Leu	Glu	Val	Gly	Ser 670	Thr	Gly
Ser	Ser	Thr 675	Ala	Glu	Thr	Val	Ser 680	Trp	Ile	Ser	Leu	Phe 685	Thr	Ala	Leu
Ser	Ser 690	Leu	Val	Phe	Thr	Leu 695	Ala	Leu	Asn	Gln	Glu 700	Ala	Leu	Gln	Asn

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Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val

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135 140 145 att cca gat gca gag cac ccc atc gga atc atc aag cca gca gga caa 595 Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile Lys Pro Ala Gly Gln ggc gac ggc caa tac cca gag ctc ctt gcc gcg cta aac gcc gac ggt 643 Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly 691 tac aac gga ttc gtc tcc atc gag cct cac ctg ggt gac ttc gat gaa Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu 739 tte qqe qqa ete tqe qqa eet gae etg tqg ace age gea tge gae get Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala 200 788 ctc gca gga atc ctg aac aac atc aac gcc gag tac aac taaggacaac Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu Tyr Asn 801 tgataatgac aaa <210> 468 <211> 226 <212> PRT <213> Corynebacterium glutamicum <400> 468 Leu Asp Ala Ala Gly Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile 150 155

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu Tyr Asn 225 <210> 469 <211> 687 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(664) <223> RXN03030 <400> 469 qaaqatgaag cagaaaagat cattggtgcg ccagaggttt ctgcattggg caacaaagca 60 caqcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat Val Leu Pro Leu Asp cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163 Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys 211 atc gac gag gtt caa cta cag ctg gaa gcc att cgc gca gaa ctc Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu 30 259 cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile 307 gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly 355 gtt tee etc tet gtt gae eet egt gee aat ggt gte gat gtg gaa ege Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403 Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe 451 acc aac cct tgg gtg ctg tct gag atc gag cct ggt gcc gct gcc gtg Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro Gly Ala Ala Ala Val 105 110

gtg Val												499
ggt Gly												547
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Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu 50 55 60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly 65 70 75 80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile 85 90 95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro 100 105 110

Gly Ala Ala Ala Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu 115 120 125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro 130 135 140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp 145 150 155 160

Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala 165 170 175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe

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Phe Ile Gly	Phe Lys Asp 170	Gly Thr Gly	Asn Ile Glu 175	His Leu Ala 180	Lys
Ile Thr Thr				ggt gga ctt Gly Gly Leu 195	
				ggc atg agc Gly Met Ser 210	
	-		-	gca ctg agc Ala Leu Ser	
•		Gln Asp Ser		aag cag aag Lys Gln Lys	
				cgc gca caa Arg Ala Gln 260	
Tyr Gly Val				gtt ggc cgc Val Gly Arg 275	
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				ggt tcc tac Gly Ser Tyr	
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Glu Ala Ala 1 35	Tyr Val Glu	His Ile Glu 40	Trp Gln Ser	Ser Tyr Pro 45	Val
Ala Gly Leu 1	Phe Ala Ala	Gly Gly Thr 55	Gly Glu Gly 60		Thr
Val Glu Glu 7	Asn His Arg 70	Val Thr Gln	Leu Ala Val 75	Gln Ala Ser	Ser 80

Pro Glu Val Pro Val Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala Ile Ala Asn Ala Gln Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu Leu Leu Pro Pro Tyr Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn 120 His Ala Ala Ala Val Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr Asn Arg Ala Asn Ala Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser Glu Arg Tyr Pro Asn Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala 235 Val Lys Gln Lys Leu Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg 250 · Asp Arg Ala Gln Gly Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys 270 Ala Val Gly Arg Asn Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu 280 Ser Glu Gln Asp Ile Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly 295 Ala Gly Ser Tyr Arg Leu Gln Leu Arg 310 <210> 473 <211> 924 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(901) <223> RXN02125

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Met Val Ala Thr Ser

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					agc Ser											163
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cgc Arg	ggc Gly	gtt Val 40	ggc Gly	gaa Glu	ggc Gly	att Ile	cgc Arg 45	acc Thr	gct Ala	gga Gly	gtg Val	ccc Pro 50	cgc Arg	gag Glu	gag Glu	259
					aag Lys											307
					gat Asp 75											355
					att Ile											403
ggt Gly	ggg Gly	gac Asp	tat Tyr 105	tca Ser	gag Glu	gga Gly	aac Asn	cgt Arg 110	gaa Glu	gcg Ala	tgg Trp	cgc Arg	gcg Ala 115	ctg Leu	gaa Glu	451
					gga Gly											499
					gag Glu											547
					ctt Leu 155											595
					tcc Ser											643
					atg Met											691
					agc Ser											739
caa Gln	ctg Leu 215	gga Gly	acg Thr	gtg Val	tct Ser	ttg Leu 220	cca Pro	aag Lys	act Thr	gcc Ala	aac Asn 225	cca Pro	gat Asp	cat His	atg Met	787
_				_	atc Ile 235	_		_					-	_	-	835

883

924

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674

145

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ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag

140

135

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					gaa Glu											691
					gac Asp											739
gcg Ala	ggc Gly 215	tta Leu	aac Asn	gtt Val	gat Asp	att Ile 220	gag Glu	atc Ile	aac Asn	tcc Ser	cgc Arg 225	ttc Phe	act Thr	tca Ser	tcc Ser	787
					tac Tyr 235											835
					aca Thr											883
					ctg Leu											931
					gcg Ala											979
aac Asn	acc Thr 295	tct Ser	gac Asp	gac Asp	ggc Gly	ttc Phe 300	atc Ile	atg Met	acc Thr	atg Met	gcc Ala 305	cgc Arg	gtg Val	tcc Ser	cag Gln	1027
					gcc Ala 315											1075
tca Ser	cca Pro	ttc Phe	ggc	gca Ala 330	cca Pro	tat Tyr	tac Tyr	gac Asp	ttg Leu 335	ctg Leu	gct Ala	ctg Leu	atg Met	gcc Ala 340	tac Tyr	1123
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					gtg Val											1219
					cgc Arg											1267
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acc att tcc ctg gca Thr Ile Ser Leu Ala 440	tca ggc ccc acc ggt Ser Gly Pro Thr Gly 445	cta atg gca gtt gct Leu Met Ala Val Ala 450	gcg 1459 Ala
ttg ctg gtc agt ttg Leu Leu Val Ser Leu 455	tcc gcg ttg att cgc Ser Ala Leu Ile Arg 460	att ctt tat agg cgc lle Leu Tyr Arg Arg 465	ttg 1507 Leu
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	Leu Ala Pro Phe Leu	gcg tct ggc acc gcg Ala Ser Gly Thr Ala 500	
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		ctg acc tgg tac cac Leu Thr Trp Tyr His 530	
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acc cgc cgt ttt gct Thr Arg Arg Phe Ala 550	gtg ctg atg ctc atg Val Leu Met Leu Met 555	gcg tgt ctg gct att Ala Cys Leu Ala Ile 560	gtg 1795 Val 565
		cca ggc gct gcg aag Pro Gly Ala Ala Lys 580	
cca tca ctg cgt ttg Pro Ser Leu Arg Leu 585	atg atg gtc att ttc Met Met Val Ile Phe 590	ggc acc atg ttc ttc Gly Thr Met Phe Phe 595	atg 1891 Met
		ttc ggt gtc tac gca Phe Gly Val Tyr Ala 610	
		gtg ggg ctg tcc tat Val Gly Leu Ser Tyr 625	gtt 1987
		tcc atc ggt gcg ttc Ser Ile Gly Ala Phe 640	

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		acc gta Thr Val	Val I							2179
		caa tcc Gln Ser								2227
		tcc atg Ser Met 715								2275
		tcc agg Ser Arg 730								2323
		ctc gtt Leu Val		Leu I						2371
		caa tac Gln Tyr	Pro A							2419
		ggc aac Gly Asn								2467
		aac gat Asn Asp 795								2515
	Ser Leu	gaa tcc Glu Ser 810	Glu A	Asp I		Gly				2563
		atc ago Ile Ser	_	Asp G	_	-	_	_	-	 2611
		act gac Thr Asp	Asp S							2659
		tcc acc Ser Thr								2707
		tcc aac Ser Asn 875	Ala A							2755

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aac ggc gtc cgc Asn Gly Val Arg 935	caa too gga Gln Ser Gly 940	Gln Ser Val	atg ctc gaa t Met Leu Glu 1 945	eac ggt cgc 2947 Tyr Gly Arg
ctt cgc gat aac Leu Arg Asp Asn 950				
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aac cta gat tct Asn Leu Asp Ser 1015	Leu Asn Asr 10	Val Ile Gly 20	Ser Glu Thr F 1025	Pro Gly Leu
ctc gac tgg gca Leu Asp Trp Ala 1030	gtt ggc ctg Val Gly Leu 1035	g caa ttc cca g Gln Phe Pro	tgc caa cgc a Cys Gln Arg 7 1040	acc ttc gac 3235 Thr Phe Asp 1045
cac tac gcc gga His Tyr Ala Gly	gtc acc gag	att cct gaa		
	1050	Ile Pro Glu 10	Tyr Arg Ile S	Ser Pro Asp 1060
cac ggc gga aaa His Gly Gly Lys 106	tcc acc ctc Ser Thr Leu	Ile Pro Glu 10 tcc cca ttc	Tyr Arg Ile S 55 caa gac tgg G	Ser Pro Asp 1060 gca ggc ggc 3331
cac ggc gga aaa His Gly Gly Lys	1050 tcc acc ctc Ser Thr Leu 5 acg gcc gaa	tcc cca ttc Ser Pro Phe 1070	Tyr Arg Ile S 55 caa gac tgg G Gln Asp Trp A aac gcc tac G	Ser Pro Asp 1060 gca ggc ggc 3331 Ala Gly Gly 1075 gaa atc ccg 3379 Glu Ile Pro
cac ggc gga aaa His Gly Gly Lys 106 gga tcc atg ggc Gly Ser Met Gly	tcc acc ctc Ser Thr Lev acg gcc gaa Thr Ala Glu aac gac tgg Asn Asp Tr	tcc cca ttc Ser Pro Phe 1070 gca gta aac Ala Val Asn 1085	Tyr Arg Ile S 55 caa gac tgg G Gln Asp Trp A aac gcc tac G Asn Ala Tyr G 109 tgg ggt tcc a	Ser Pro Asp 1060 gca ggc ggc 3331 Ala Gly Gly 1075 gaa atc ccg 3379 Glu Ile Pro 90 atc gaa cgc 3427
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Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His 1130 1135 1140

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3561

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Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser 35 40 45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val 50 55 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala 85 90 95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu 100 105 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly
115 120 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly 130 135 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp 145 150 155 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu 165 170 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro 180 185 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala 195 200 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser 210 215 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile 225 230 235 240

Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp 245 250 255

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His	Phe 290	Leu	Gly	Ala	Asn	Thr 295	Ser	Asp	Asp	Gly	Phe 300	Ile	Met	Thr	Met
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Phe	Gly	Val	Pro	Glu 325	Ser	Pro	Phe	Gly	Ala 330	Pro	Tyr	Tyr	Asp	Leu 335	Leu
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Thr	Arg	Pro	Glu	Pro 405	Ile	Ile	Ala	Met	Gly 410	Ala	Leu	Leu	Ala	Trp 415	Val
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Met	Ala 450	Val	Ala	Ala	Leu	Leu 455	Val	Ser	Leu	Ser	Ala 460	Leu	Ile	Arg	Ile
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Ser	Lys	Val	Phe	Gly 485	Ala	Ser	Met	Ala	Met 490	Leu	Ala	Pro	Phe	Leu 495	Ala
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Thr	Val	Met 515	Glu	Ser	Ile	Ser	Val 520	Arg	Ser	Ala	Lys	Gly 525	Pro	Ala	Leu
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Val 545	Asp	Gly	Ser	Phe	Thr 550	Arg	Arg	Phe	Ala	Val 555	Leu	Met	Leu	Met	Ala 560
Cys	Leu	Ala	Ile	Val 565	Val	Ile	Ala	Ile	Leu 570	Arg	Tyr	Gly	Arg	Ile 575	Pro

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900 905 910

Ala Thr Glu Glu Ala Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile 915 920 925

Glu His Tyr Asp Ile Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met 930 935 940

Leu Glu Tyr Gly Arg Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly 945 950 955 960

Glu Ala Met Met Tyr Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu 965 970 975

Arg Tyr Pro Leu Asp Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile 980 985 990

Val Ala Thr Asp Val Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr 995 1000 1005

Pro Pro Arg Val Pro Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser 1010 1015 1020

Glu Thr Pro Gly Leu Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys 1025 1030 1035 1040

Gln Arg Thr Phe Asp His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr 1045 1050 1055

Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln 1060 1065 1070

Asp Trp Ala Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn 1075 1080 1085

Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp 1090 1095 1100

Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala 1105 1110 1115 1120

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<210> 477

<211> 1509

<212> DNA

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<222> (101)..(1486)

<223> RXN01175

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cct acg tgg gat cgt gca cag gca gaa aac gtg Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val 40 45	g cgc aag atc ctt gag 259 Arg Lys Ile Leu Glu 50
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gat atc gtc aac ggt gtg gag gca acc cca gag Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu 150 155	ı Ala Arg Arg His Asp
cct gcc cgc atg atc cgt gct tac gct aac gct Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala 170	
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agc gag tgg aac cgc gag ttc gtt gcg aac tcc Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser 200 205	
tac gag gct ctt gct cgt gag atc gac tcc ggt Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly 215 220	
gca tgt ggc gtg tcc gat gag tcc ctg cgt gct	gca gat atc tac tgc 835

Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr C 230 235 240 2	Cys 245
tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt c Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg L 250 255 260	
gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct c Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala H 265 270 275	
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aac ttc gca tcc atg atc tct aac cca atc ggc atc aag att ggt c Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly P 295 300 305	
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Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val 35 40 45

Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val 50 55 60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe 65 70 75 80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu 85 90 95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val 100 105 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala 115 120 125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu 130 135. 140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu 145 150 155 160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala 165 . 170 . 175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala 180 185 190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser 195 200 205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly 210 215 220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala 225 230 240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg 245 250 255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr 260 265 270

Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met 275 280 285

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Arg	Met	Gly	His 340	Asp	Lys	Val	Arg	Ser 345	Val	Leu	Pro	Gly	Val 350	Ile	Gln	
Ala	Val	Glu 355	Ala	Ser	Gly	His	Lys 360	Val	Ile	Trp	Gln	Ser 365	Asp	Pro	Met	
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Pro	Gly	Arg 435	Tyr	Glu	Ser	Ala	Cys 440	Asp	Pro	Arg	Leu	Asn 445	Thr	Gln	Gln	
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	aaa Lys															163
	gac Asp															211
	gag Glu															259

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	gtc Val 215															787
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Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn 50 60

Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp
65 70 75 80

Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp 85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly 100 105 110

Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser 115 120 125

Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu 130 135 140

Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp 145 150 155 160

Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys 165 170 175

Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu 180 185 190

Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val 195 200 205

Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His 210 215 220

Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala 225 230 235 240

His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro 245 250 255

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	cac His															691
	cca Pro															739
	acc Thr 215															787
	ggt Gly															835
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	cga Arg															931
	atc Ile	Āla			_		Ala	-	_		_	Pro				979
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Val 145	Lys	Leu	Ala	Leu	Glu 150	Ala	Thr	Pro	Phe	Ser 155	His	Leu	Lys	Thr	Ile 160	
Tyr	Asp	Ala	Leu	Glu 165	Val	Val	Ser	His	Ser 170	Asp	Ser	Pro	Ser	Ala 175	Gly	
Leu	Met	Val	Asp 180	Ile	Trp	His	Thr	Ala 185	Lys	Ile	Gly	Ile	Pro 190	Asn	Asp	
Glu	Leu	Trp 195	Arg	Asn	Ile	Pro	Leu 200	Ser	Lys	Val	Asn	Ala 205	Val	Glu	Val	
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				gct Ala 10												163
				acc Thr												211

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45

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Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly
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att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt

Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu

105

110

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Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly
135 140 145

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Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr
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Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His
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His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg

Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg

His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser 250

PCT/IB00/00943 WO 01/00844

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547 ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att

694

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	agt Ser															643
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	gat Asp															739
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	act Thr															835
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<400> 486

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Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu 35 40 45

Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His 50 55 60

Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu 65 70 75 80

Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp 85 90 95

Val Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro 100 105 110

Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe 115 120 125

Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly 130 135 140

Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr 145 150 155 160

Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val 165 170 175

Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr 180 185 190

Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu 195 200 205

Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu 210 215 220

Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu 225 230 235 240

Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala 245 250 255

Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser 260 265 270

Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe 275 280 285

Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala 290 295 300

Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp

315

320

310

305

Ala His His Ala His Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu 330 325 Leu Val Val Pro Leu Gly His Gly Asp Val Ala Glu Gln Gly 340 345 <210> 487 <211> 1248 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1225) <223> RXS00584 <400> 487 tagttqtqcc acctaaaacq cqaacaqaac cqqaqtcqaq cagcacctcc ccgcaagggt 60 agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa Met His Ser Pro Glu agg caa gaa aaa atg agt tet eea gte tea ete gaa aac geg geg tea 163 Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser 10 acc agc aac aag ege gte gtg get tte eac gag etg eet age eet aca 211 Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr 25 gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259 Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val 45 gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac. Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp 55 60 ege etc gtt gtc gtt gtg gga eet tge tea gtt eac gat eet gaa gea Arg Leu Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala 70 75 80 ged atd gat tad gea aad egd etg get eeg etg gea aag egd ett gat Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp 100 90 95 cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451 Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr 105 110 atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr 120 125 tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547 Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp 135 140 145

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														ggc Gly 180		643
cgt Arg	acc Thr	acc Thr	gaa Glu 185	tct Ser	cag Gln	gtg Val	cac His	cgc Arg 190	cag Gln	ctg Leu	gct Ala	tct Ser	ggg Gly 195	atg Met	tct Ser	691
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														gca Ala		1075
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Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
35 40 45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe 50 55 60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Gly Pro Cys Ser Val 65 70 75 80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu 85 90 95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe 100 105 110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro 115 . 120 125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg 130 135 140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu 145 150 155 160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp 165 170 175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu 180 185 190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly 195 200 205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Gln Asn Pro His 210 215 220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr 225 230 235 240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly
245 250 255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly 260 265 270

Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys 275 280 285

Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile 295 Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu 315 310 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly 325 330 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp 345 Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg 360 355 Glu Arg Arg Ala Ala Lys 370 <210> 489 <211> 1131 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1108) <223> RXS02574 <400> 489 tqtqctcctt qcqqqctqcq caqaaqaqcc ggaacagcaa aaagcaataa gccgcttatc 60 gacgtccccc tccacccctc ccgcaccgac cgcggaggat ttg gcg cgc gcg caa 115 Leu Ala Arg Ala Gln atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly 10 qtt qcq aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly 25 30 35 259 ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro 40 45 307 ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser 55 60 355 qtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile 70 75 ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro 100 90 95 451 qaa caa qta qaa gat ctc gca gaa atc cta ggc act ggt tta gct gca

Glu	Gln	Val	Glu 105	Asp	Leu	Ala	Glu	Ile 110	Leu	Gly	Thr	Gly	Leu 115	Ala	Ala	
														gct Ala		499
														gcc Ala		547
-	_			-		•		_	_			_		gta Val		595
														agt Ser 180		643
_	-				-		-			-		_		ctt Leu		691
														gac Asp		739
														gac Asp		787
														agt Ser		835
														gac Asp 260		883
														gaa Glu		931
														atc Ile		979
		-	_					-	_	-	-	-		gtt Val		1027
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<212> PRT

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<400> 490

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Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val 50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly 100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
115 120 125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser 130 135 140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly 145 150 155 160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
165 170 175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala 180 185 190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu 195 200 205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly 210 215 220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln 225 230 235 240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val 245 250 255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln 275 280 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val 290

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala 305

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys 325

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703

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His 145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp 165 170 175	528
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu 180 185 190	576
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu 195 200 205	624
gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly 210 215 220	672
gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu 225 230 235 240	720
gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg 245 250 255	768
ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu 260 265 270	816
ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile 275 280 285	864
tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu 290 295 300	912
cac aat atg cag ctc att gat gct gta tca cag tca gct gca ggt His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly 305 310 315 320	960
ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn 325 330 335	1008
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ctg tca gac acc Leu Ser Asp Thr 35				
cgt gca gca aca Arg Ala Ala Thr 50				
cgt tcc cca ggc Arg Ser Pro Gly 65	gtg gca cac a Val Ala His 70	Ile Arg Asp L	etc gtg cag tcc eu Val Gln Ser 75	ggc gag 240 Gly Glu 80
ctt ggc aag gtt Leu Gly Lys Val				
tcc aat gca cag Ser Asn Ala Gln 100	Ala Pro Ile			
tcc ggc gca ctg Ser Gly Ala Leu 115	Ala Asp Val			
ttc gtt gca gga Phe Val Ala Gly 130				
acc gtg atc acc Thr Val Ile Thr 145		Lys Pro Leu G		
gaa ggc ggc gca Glu Gly Gly Ala				
att gca tca ttc Ile Ala Ser Phe 180	Ser Gly Ser		gc gga acc gca ly Gly Thr Ala 190	
cag gtc agc cgc	att tcc cag	gga cac cca a	ac acc cta ggt	ttt gaa 624

Gln	Val	Ser 195	Arg	Ile	Ser	Gln	Gly 200	His	Pro	Asn	Thr	Leu 205	Gly	Phe	Glu	
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	ttc Phe															720
_	ggc Gly		-							_					_	768
	ggc Gly															816
	ttc Phe															864
	gaa Glu 290															912
	aat Asn															960
	gaa Glu															1008
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1	Asp	vaı	vaı	Ser 5	vaı	vaı	vaı	Ala	10	rne	Leu	HIS	Arg	15	TIE	
Val	Glu	Ala	Leu 20	Leu	Ala	Ser	Gly	Lys 25	His	Val	Leu	Cys	Glu 30	Lys	Pro	
Leu	Ser	Asp 35	Thr	Ile	Glu	Asp	Ala 40	Glu	Ala	Met	Ile	Glu 45	Ala	Ala	Gly	
Arg	Ala 50	Ala	Thr	Asn	Gly	Thr 55	Ile	Ala	Arg	Ile	Gly 60	Leu	Thr	Tyr	Arg	
Arg 65	Ser	Pro	Gly	Val	Ala 70	His	Ile	Arg	Asp	Leu 75	Val	Gln	Ser	Gly	Glu 80	
Leu	Gly	Lys	Val	Leu 85	His	Val	Thr	Gly	His 90	Tyr	Trp	Thr	Asp	Tyr 95	Gly	

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu 120 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu Gln Val Ser Arq Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu 235 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu 265 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile 280 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Gly Leu 295 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly 315 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn

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<213> Corynebacterium glutamicum

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<223> RXS03224

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Phe Ile Gly Asn H		c cgc att gcc acc r Arg Ile Ala Thr 255		883
		g atc ctc ttc acg a Ile Leu Phe Thr 270		931
-		g cag ggc ttt acg u Gln Gly Phe Thr 5		979
		c att agg cca cct a Ile Arg Pro Pro 305		1027
		t gaa aac att tat e Glu Asn Ile Tyr 320		1075
Ala Leu Arg Arg G		g ttg tat cag gcg p Leu Tyr Gln Ala 335		1123
		g acc tat aag tcc t Thr Tyr Lys Ser 350		1171
		t gat ttg gaa gag u Asp Leu Glu Glu 5		1219
		g ttt cag tac agc u Phe Gln Tyr Ser 385		1268
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Arg Leu Pro Asn I		p Leu Asp Tyr Val 0	Val Glu Leu Gly 45	
Cys Asn Ala Leu M 50	et Leu Gly Pr 55	o Val Phe Glu Ser 60	Val Ser His Gly	

Tyr 65	Asp	Thr	Leu	Asp	Phe 70	Tyr	Arg	Ile	Asp	Pro 75	Arg	Leu	Gly	Thr	Glu 80
Glu	Asp	Met	Asp	Ala 85	Leu	Leu	Glu	Ala	Ala 90	Asn	Gln	Arg	Gly	Ile 95	Gly
Val	Leu	Phe	Asp 100	Gly	Val	Phe	Asn	His 105	Val	Ser	Ser	Ser	Ser 110	Lys	Tyr
Leu	Asp	Leu 115	Thr	Thr	Gly	Ala	Ser 120	Phe	Glu	Gly	His	Asp 125	Ile	Leu	Ala
Glu	Leu 130	Asp	His	Thr	Asn	Pro 135	Ala	Val	Val	Asp	Leu 140	Val	Val	Asp	Va]
Met 145	Asn	His	Trp	Leu	Asp 150	Arg	Gly	Ile	Ala	Gly 155	Trp	Arg	Leu	Asp	Ala 160
Val	Tyr	Ala	Ile	Ala 165	Pro	Glu	Phe	Trp	Glu 170	Lys	Val	Leu	Pro	Glu 175	Val
Arg	Arg	Lys	His 180	Pro	His	Ala	Trp	Ile 185	Val	Gly	Glu	Met	Ile 190	His	Gly
Asp	Tyr	Ser 195	Asp	Tyr	Val	Lys	Ser 200	Ser	Gly	Ile	Asp	Ser 205	Val	Thr	Glu
Tyr	Glu 210	Leu	Trp	Lys	Ala	Ile 215	Trp	Ser :	Ser	Ile	Lys 220	Glu	Arg	Asn	Phe
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Phe	Val	Pro	Gln	Thr 245	Phe	Ile	Gly	Asn	His 250	Asp	Val	Thr	Arg	Ile 255	Ala
Thr	Arg	Ile	Gly 260	Gln	Ser	Asn	Ala	Ile 265	Leu	Ala	Ala	Ala	11e 270	Leu	Phe
Thr	Val	Gly 275	Gly	Thr	Pro	Ser	Ile 280	Tyr	Tyr	Gly	Asp	Glu 285	Gln	Gly	Phe
Thr	Gly 290	Leu	Lys	Glu	Asp	Asn 295	Val	Phe	Gly	Asp	Asp 300	Ala	Ile	Arg	Pro
Pro 305	Leu	Pro	Ala	Glu	Phe 310	Ser	Pro	Leu	Gly	Thr 315	Trp	Ile	Glu	Asn	11e 320
Tyr	Lys	Ala	Leu	Ile 325	Ala	Leu	Arg	Arg	Gln 330	His	Pro	Trp	Leu	Tyr 335	Glr
Ala	His	Thr	Glu 340	Val	Leu	Glu	Ile	Ala 345	Asn	Glu	Ala	Met	Thr 350	Tyr	Lys
Ser	Val	Gly 355	Leu	Gly	Gly	Glu	Glu 360	Leu	Thr	Val	His	Leu 365	Asp	Leu	Glu
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Ser Ala 385

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gtg Val	aaa Lys	agc Ser 200	tcc Ser	ggc Gly	att Ile	gat Asp	tcc Ser 205	gtt Val	acc Thr	gaa Glu	tac Tyr	gaa Glu 210	ctg Leu	tgg Trp	aaa Lys	739
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					aat Asn 235											835
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					gcc Ala											931
	_				ggc Gly	_		-			_		_			979
					gac Asp											1027
					acc Thr 315											1075
					cac His											1123
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<400> 498

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Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
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Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly 50 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu 65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly 85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala 115 120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
130 135 .140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala 145 150 155 160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val 165 170 175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
180 185 190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu 195 200 205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe 210 215 220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr 225 230 235 240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala 245 250 255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ile Leu Phe 260 265 270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe 275 280 285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro 290 295 300

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile 310 315 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln 330 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys 345 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu 360 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr 375 Ser Ala 385 <210> 499 <211> 517 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(517) <223> RXC00233 <400> 499 cgcctccagc agttgaggga gaagttccaa cacttgcacc aactgaggaa gcaactgtgc 60 aataqcqctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa Met Ser Val Asn Glu 1 qca qat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly 20 10 211 gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val 35 25 atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr 40 tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val 55 gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu 70 75 ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg 100 90 95 451 aac qca att gaa gat ctc qqc acg gat ttt tcc ggc ggt ggc atg cct

Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Met Pro gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu 125 517 ggc cca cac cat ttc ctt Gly Pro His His Phe Leu 135 <210> 500 <211> 139 <212> PRT <213> Corynebacterium glutamicum <400> 500 Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala 55 Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His 85 90 Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp 115 120 Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu 130 <210> 501 <211> 849 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(826) <223> RXC00236 <400> 501 aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60 agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt Met Val Ile Ser Phe

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163 Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211 Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro 403 qgc tqc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu 90 acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451 Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu 105 gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp 125 120 ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu 135 gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile 150 155 160 ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val 170 gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu 185 ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala 200 gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg 215 220 gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa Asp Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile 230 235

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<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly 50 . 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr 130 135 140

Asp Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro 225 230 235 240

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190 195 185 ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln 200 cag get gtt gaa get ete gge gat gtt gat gte ate tae gtt eea aet 787 Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr gac aac atg gtt gtt tee ggt att tet tet etg gtt cag gtt get gag 835 Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu caq aaq caq atc cct qtq atc qqc qct qaq tcc qqc act qtt gag ggt 883 Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly qqc qca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag 931 Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln 979 act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala 280 acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa 1027 Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu 300 295 gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp 310 315 320 aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga 1113 Lys Ala Glu Arg Val 330 <210> 504 <211> 330 <212> PRT <213> Corynebacterium glutamicum <400> 504 Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala 70

Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser

85 90 95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
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Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu 145 150 155 160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr 165 170 175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys 180 185 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr 195 200 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val 210 215 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu 225 230 235 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser 245 250 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr 260 265 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp 275 280 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr 290 295 300

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ggc ggc atg gac aa: Gly Gly Met Asp Ly: 135				
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Pro	Val	Asp	Glu	Tyr 325	Leu	Arg	Glu	Gly	Gly 330	Pro	Ala	Val	Ile	Asp 335	Thr
Ala	His	Trp	Ala 340	Ser	Glu	Phe	Pro	Trp 345	Thr	Ser	Gln	Ala	Gln 350	Glu	Ile
Leu	Gln	Asp 355	Lys	Ala	Pro	Gln	Val 360	Glu	Val	Asp	Val	Ile 365	Ser	Ile	Arç
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<213> Corynebacterium glutamicum

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Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Phe

185

						aaa Lys										739
						atg Met 220										787
						ccc Pro										835
						gga Gly										883
						cca Pro										931
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		_	_	-		caa Gln 300		-		-			_	_		1027
tct Ser 310	gcg Ala	ctt Leu	gca Ala	gca Ala	gcg Ala 315	aac Asn	atc Ile	atg Met	gaa Glu	gaa Glu 320	ctg Leu	ggt Gly	gtt Val	ggc Gly	ccg Pro 325	1075
						gat Asp										1123
						atg Met										1171
		_			_	gcg Ala			-		-	-	-		_	1219
						cca Pro 380										1267
						gca Ala										1315
						gat Asp										1363
						gtc Val										1411

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1470

aaaatgaact caa

<210> 508

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

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Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly 85 90 95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala 100 105 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro 115 120 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val 130 135 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met 145 150 155 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln 165 170 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg 180 185 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr 195 200 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp 210 215 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr 225 230 235 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser 245 250 255

Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala 280 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu 310 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu 325 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro 360 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr 440 Gly <210> 509 <211> 1203 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1180) <223> RXC00412 <400> 509 cttttgacga acaccacgtc gcgtacgctt cctcggggcg ttaaactatt tgtcttccag 60 cttttqtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg Val Ser His Thr Ala tec aca ecg acg eca gag gaa tae tee geg eag eaa eec age ace eag Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln 10 15

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						gcg Ala										259
						atc Ile 60										307
act Thr 70	ctt Leu	gtc Val	cgc Arg	ctc Leu	atc Ile 75	aat Asn	ggc	ctt Leu	gac Asp	tcc Ser 80	ccc Pro	acg Thr	agc Ser	ggt Gly	tcg Ser 85	355
ttg Leu	ctg Leu	ctc Leu	aac Asn	ggc Gly 90	acc Thr	gac Asp	atc Ile	gtc Val	gga Gly 95	atg Met	ccc Pro	gag Glu	tct Ser	aag Lys 100	ctg Leu	403
cgt Arg	aaa Lys	ctg Leu	cgc Arg 105	agt Ser	aat Asn	atc Ile	ggc Gly	atg Met 110	att Ile	ttc Phe	cag Gln	cag Gln	ttc Phe 115	aac Asn	ctg Leu	451
ttc Phe	cag Gln	tcg Ser 120	cgt Arg	act Thr	gcg Ala	gct Ala	gga Gly 125	aat Asn	gtg Val	gag Glu	tac Tyr	ccg Pro 130	ctg Leu	gaa Glu	gtt Val	499
gcc Ala	aag Lys 135	atg Met	gac Asp	aag Lys	gca Ala	gct Ala 140	cgt Arg	aaa Lys	gct Ala	cgc Arg	gtg Val 145	caa Gln	gaa Glu	atg Met	ctc Leu	547
gag Glu 150	ttc Phe	gtc Val	ggc Gly	ctg Leu	ggc Gly 155	gac Asp	aaa Lys	ggc Gly	aaa Lys	aac Asn 160	tac Tyr	ccc Pro	gag Glu	cag Gln	ctg Leu 165	595
tcg Ser	ggc Gly	ggc Gly	cag Gln	aag Lys 170	cag Gln	cgc Arg	gtc Val	ggc Gly	att Ile 175	gcc Ala	cgt Arg	gca Ala	ctg Leu	gcc Ala 180	acc Thr	643
		Thr		Leu	Leu	gcc Ala	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp		691
						ctg Leu										739
ctg Leu	ggc Gly 215	atc Ile	acc Thr	atc Ile	gtt Val	gtg Val 220	atc Ile	acc Thr	cac His	gaa Glu	atg Met 225	gaa Glu	gtt Val	gtg Val	cgt Arg	787
						gct Ala										835
						gtg Val										883
caa	aag	ttc	gtg	gcc	acc	gcg	ctg	cgt	aac	acc	сса	gac	caa	gtg	gaa	931

GIN DYS FNE	Val A. 265	la Thr	Ala	Leu	Arg 270	Asn	Thr	Pro	Asp	Gln 275	Val	Glu	
tcg gaa gat Ser Glu Asp 280	Leu L												979
act gaa acg Thr Glu Thr 295													1027
ggt gct ttt Gly Ala Phe 310													1075
caa tca ttt Gln Ser Phe	Gly L												1123
att gaa gag Ile Glu Glu													1171
atc acc cga Ile Thr Arg 360	_	gagat g	gated	tcgc	ca go	et							1203
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<212> PRT <213> Coryr	ebacte	rium gl	lutam	nicum	n								
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<213> Coryn		-				Pro 10	Glu	Glu	Tyr	Ser	Ala 15	Gln	
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Val 145	Gln	Glu	Met	Leu	Glu 150	Phe	Val	Gly	Leu	Gly 155	Asp	Lys	Gly	Lys	Asn 160	
Tyr	Pro	Glu	Gln	Leu 165	Ser	Gly	Gly	Gln	Lys 170	Gln	Arg	Val	Gly	Ile 175	Ala	
Arg	Ala	Leu	Ala 180	Thr	Asn	Pro	Thr	Leu 185	Leu	Leu	Ala	Asp	Glu 190	Ala	Thr	
Ser	Ala	Leu 195	Asp	Pro	Glu	Thr	Thr 200	His	Glu	Val	Leu	Glu 205	Leu	Leu	Arg	
Lys	Val 210	Asn	Arg	Glu	Leu	Gly 215	Ile	Thr	Ile	Val	Val 220	Ile	Thr	His	Glu	
Met 225	Glu	Val	Val	Arg	Ser 230	Ile	Ala	Asp	Lys	Val 235	Ala	Val	Met	Glu	Ser 240	
Gly	Lys	Val	Val	Glu 245	Tyr	Gly	Ser	Val	Tyr 250	Glu	Val	Phe	Ser	Asn 255	Pro	
Gln	Thr	Gln	Val 260	Ala	Gln	Lys	Phe	Val 265	Ala	Thr	Ala	Leu	Arg 270	Asn	Thr	
Pro	Asp	Gln 275	Val	Glu	Ser	Glu	Asp 280	Leu	Leu	Ser	His	Glu 285	Gly	Arg	Leu	
Phe	Thr 290	Ile	Asp	Leu	Thr	Glu 295	Thr	Ser	Gly	Phe	Phe 300	Ala	Ala	Thr	Ala	
Arg 305	Ala	Ala	·Glu	Gln	Gly 310	Ala	Phe	Val	Asn	Ile 315	Val	His	Gly	Gly	Val 320	
Thr	Thr	Leu	Gln	Arg 325	Gln	Ser	Phe	Gly	Lys 330	Met	Thr	Val	Arg	Leu 335	Thr	
Gly	Asn	Thr	Ala 340	Ala	Ile	Glu	Glu	Phe 345	Tyr	Gln	Thr	Leu	Thr 350	Lys	Thr	
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cgt1	ttct	gee a	aagca	aaac	eg to	ggco	caggt	t gat	tttaq	geet		agc Ser				115
atg	cga	aat	att	gtc	aag	acc	tac	aac	att	gga	tct	gaa	ggt	gaa	ctc	163

Met	Arg	Asn	Ile	Val 10	Lys	Thr	Tyr	Asn	Ile 15	Gly	Ser	Glu	Gly	Glu 20	Leu	
acc Thr	gtg Val	ttg Leu	cac His 25	ggt Gly	gtg Val	gat Asp	ttc Phe	cat His 30	gtg Val	gac Asp	cgt Arg	ggc Gly	gaa Glu 35	ttc Phe	gtg Val	211
tcg Ser	gtt Val	gtg Val 40	ggt Gly	acg Thr	tcc Ser	ggc Gly	tca Ser 45	ggt Gly	aaa Lys	tca Ser	acg Thr	atg Met 50	atg Met	aac Asn	atc Ile	259
att Ile	ggg Gly 55	ttg Leu	ttg Leu	gat Asp	aag Lys	cca Pro 60	act Thr	gat Asp	ggc Gly	acg Thr	tac Tyr 65	acc Thr	ttg Leu	gat Asp	ggc Gly	307
gtg Val 70	gat Asp	gtg Val	ttg Leu	gat Asp	atc Ile 75	agc Ser	gat Asp	gat Asp	gct Ala	ttg Leu 80	gcg Ala	agc Ser	cac His	cgc Arg	gct Ala 85	355
aaa Lys	tcg Ser	att Ile	ggt Gly	ttt Phe 90	gtg Val	ttt Phe	cag Gln	aac Asn	ttc Phe 95	aat Asn	ctg Leu	att Ile	ggc Gly	cgg Arg 100	atc Ile	403
gat Asp	gcg Ala	ttg Leu	aag Lys 105	aat Asn	gtg Val	gaa Glu	atg Met	ccc Pro 110	atg Met	atg Met	tat Tyr	gcg Ala	ggc Gly 115	att Ile	ccg Pro	451
gct Ala	aag Lys	cag Gln 120	cgg Arg	aga Arg	agt Ser	Arg	gcg Ala 125	gtt Val	gaa Glu	tta Leu	ttg Leu	gaa Glu 130	atg Met	gtc Val	Gly ggg	499
				ctc Leu												547
				gcc Ala												595
				gaa Glu 170												643
atg Met	gtg Val	atg Met	gat Asp 185	att Ile	ttc Phe	cac His	cag Gln	ctc Leu 190	aac Asn	aag Lys	gag Glu	cag Gln	ggc Gly 195	aaa Lys	acc Thr	691
				act Thr												739
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tca Ser 230	tga	gcct	tgc (agaat	tcaa	tt c	tt									813

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- <212> PRT
- <213> Corynebacterium glutamicum

<400> 512

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- Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp 20 25 30
- Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser 35 40 45
- Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr 50 55 60
- Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
 65 70 75 80
- Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn 85 90 95
- Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met 100 105 110
- Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu 115 120 125
- Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu 130 135 140
- Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala 145 150 155 160
- Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp 165 170 175
- Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys 180 185 190
- Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala 195 200 205
- Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly 210 215 220
- Ser Glu Val Lys His Ser 225 230
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- <223> RXC01004

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220 225 215 ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct 931 Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala qat cct qaq atg qat ccc tcc gag acc att ccg cgt tct gca ctg cgc 979 Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg 1027 cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt 1075 Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg 1123 Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val 340 ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt 1172 Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp aactgtgttg gac 1185 <210> 514 <211> 354 <212> PRT <213> Corynebacterium glutamicum <400> 514 Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile 105 Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala 120 Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val 250 Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met 295 Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln 305 310 315 Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu 330 Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser 345 340

Asp Asp

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					acc Thr											163
					gaa Glu											211
					gtc Val											259
tac Tyr	aag Lys 55	gag Glu	cgc Arg	atg Met	aag Lys	gct Ala 60	gca Ala	tgg Trp	gga Gly	cca Pro	gca Ala 65	cgc Arg	gtt Val	ttc Phe	gca Ala	307
					cat His 75											355
					cac His											403
					gca Ala											451
-			-	-	gca Ala	-			-		_	-	_		_	499
					gca Ala											547
					ggc Gly 155											595
					gag Glu											643
					ccc Pro											691
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<211> 203

<212> PRT

<213> Corynebacterium glutamicum

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Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro 50 55 60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly 65 70 75 80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly 85 90 95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu 100 105 110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp 115 120 125

Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly 130 135 140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe 145 150 155 160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile 165 170 175

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Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr 50 55 60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg 65 70 75 80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu 85 90 95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro 100 105 110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu 115 120 125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp 130 135 140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu 145 150 155 160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu 165 170 175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His 180 185 190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn 195 200 205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg 210 215 220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gln Val Glu Leu 225 230 235 240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg 245 250 255

Ile Ala Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
260 265 270

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		gca tct cca ttt acg c Ala Ser Pro Phe Thr H 225	
		gcc gca gct cag cgc a Ala Ala Ala Gln Arg S 240 2	
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		tcg cca gac gag aag g Ser Pro Asp Glu Lys A 275	
tcg aag tgg tct cgc Ser Lys Trp Ser Arg 280	cca atc ctc acc gtt Pro Ile Leu Thr Val 285	gct gag acc gac acg t Ala Glu Thr Asp Thr I 290	ta 979 Leu
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cat His	ccg Pro	gtg Val	aac Asn 105	cgg Arg	agt Ser	gcg Ala	cgg Arg	atc Ile 110	gcg Ala	gaa Glu	cag Gln	aag Lys	gtt Val 115	cac His	cgc Arg	451
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747

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gac gat ata t Asp Asp Ile P 130											432
ccg ttt agg g Pro Phe Arg A 145	la Val V										480
gcc atg gcg c Ala Met Ala G											528
gca ctg cgt t Ala Leu Arg L 1	tg ctg g eu Leu V 80	tg cgc al Arg	gga cad Gly Gli 18	Ser	gcc Ala	acg Thr	acc Thr	tat Tyr 190	tcc Ser	att Ile	576
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Trp Val Leu 3	Ala Glu Thr	Ile Lys Gly	Ser Thr Pro	Ser Asp Trp 45	Glu
Glu Ile Leu 7	Arg Pro Leu	Ala Leu Leu 55	Thr Asp Ala 60	Ser Phe Thr	Leu
Pro Pro Arg 8	Ser Thr Arg 70		Leu Asp Leu 75	Lys His Leu	Glu 80
Pro Ser Arg	Leu Lys Pro 85	Glu Gln Pro	Glu Lys Pro 90	Ala Phe Thr 95	Pro
	Glu Glu Asp 100	Leu Ser Gln 105	Pro Leu Val	Ile Arg Pro 110	Glu
Glu Pro Leu (Gln Met Pro	Val Arg Gly 120	Val Gln Glu	Ser Arg Gly 125	Val
Val Glu Pro 1	Arg Ser Leu	Gly Ala Asp 135	Asp Val Glu 140	Ser Ile Ala	Glu
Gly Asp Pro 0 145	Glu Arg Pro 150		Tyr Gly Thr 155	Arg Val Leu	Arg 160
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Val Asn Ala Trp Asn Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp 130 135 140

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His Gly Val Lys Val Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe 165 170 175

Asn Ser Ala Asp Val His Lys Leu Ile Asp Leu Thr Gly Ala Thr His 180 185 190

Val Gly Val Glu Leu Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp 195 200 205

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Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu 85 90 95

Leu Pro Thr Pro Asp Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
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His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro 115 120 125

Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu 130 135 140

Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu 145 150 155 160

Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala 165 170 175

Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn 180 185 190

Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro 195 200 205

Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys 210 215 220

Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr 225 230 235 240

Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala 245 250 255

Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln 260 265 270

Ala Val Leu Glu Met Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp 275 280 285

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_		-			_				_	gac Asp		_			595
										aat Asn					643
										gag Glu					691
										ggc					739
		_	_			_		_	_	tat Tyr 225				-	787
										gaa Glu					835
										gat Asp					883
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aago	gttt	tt t	cg												942

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<213> Corynebacterium glutamicum

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Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg 145 150 155 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala 165 170 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala 195 200 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala 210 215 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu 225 230 235 240

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Ala

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Met Ala Lys Ile Ile

1 5

tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag

Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys

10

20

ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc $$ 211 Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr $$ 35

cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259 Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg 40 45 50

ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307 Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu 55 60 65

ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc 355 Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser 70 80 85

gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln
90 95 100

ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa 451 Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu 105 110 115

aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac 499 Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn 120 125 130

cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc

Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val

135

140

145

aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca 595 Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala 150 165

gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His 170 175 180

aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys
185
190
195

cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag 739

His	Ile	Ala 200	Ala	Asp	Gly	Thr	Glu 205	Thr	Ile	Leu	Lys	Asp 210	Ser	Leu	Lys	
					gtt Val											787
_	-	-			ctc Leu 235		_	-	-	-	-	_	-			835
				-	cac His	_	_	-		-	_	_	-		-	883
					cac His											931
					cag Gln											979
		-	-		ctc Leu			_			_	_			-	1027
					ttc Phe 315											1075
					gct Ala											1123
					gct Ala											1171
	-				gac Asp	-	_		-	-		_	-			1219
					gct Ala											1267
					ttc Phe 395											1315
					cag Gln											1363
					gca Ala											1411
					gag Glu											1459

445 450 440 gca tgc cag gtc aag gat gcc cca atc cag gat tgg gta aag ctt gct 1507 Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala 455 460 gtc acc cgc tcc cgt ctc tcc gga atg cct gca gtg ttc tgg ttg gat 1555 Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp 475 cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac 1603 Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr 490 ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct 1651 Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro 1699 gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp 530 525 acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu 535 540 1795 ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val 555 560 550 cct ttg atg gct ggc gga ctg ttc gag acc ggt gct gga tct 1843 Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser 575 570 gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg 1891 Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp 585 gat too etc ggt gag tto etc gea etg get gag tee tte ege eac gag 1939 Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu 600 605 ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg 1987 Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu 615 gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc 2035 Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg 630 635 aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag 2083 Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys 650 ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct 2131

2179

Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala

gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp 685

665

680

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Thr	Tyr	Ser	Leu 20	Lys	Pro	Val	Val	Glu 25	Ala	Phe	Ala	Ala	Thr 30	Ala	Gly	
Ile	Glu	Val 35	Glu	Thr	Arg	Asp	Ile 40	Ser	Leu	Ala	Gly	Arg 45	Ile	Léu	Ala.	• •
Gln	Phe 50	Pro	Glu	Arg	Leu	Thr 55	Glu	Asp	Gln	Lys	Val 60	Gly	Asn	Ala	Leu	
Ala 65	Glu	Leu	Gly	Glu	Leu 70	Ala	Lys	Thr	Pro	Glu 75	Ala	Asn	Ile	Ile	Lys 80	
Leu	Pro	Asn	Ile	Ser 85	Ala	Ser	Val	Pro	Gln 90	Leu	Lys	Ala	Ala	Ile 95	Lys	
Glu	Leu	Gln	Asp 100	Gln	Gly	Tyr	Asp	Ile 105	Pro	Glu	Leu	Pro	Asp 110	Asn	Ala	
Thr	Thr	Asp 115	Glu	Glu	Lys	Asp	Ile 120	Leu	Ala	Arg	Tyr	Asn 125	Ala	Val	Lys	
Gly	Ser 130	Ala	Val	Asn	Pro	Val 135	Leu	Arg	Glu	Gly	Asn 140	Ser	Asp	Arg	Arg	
Ala 145	Pro	Ile	Ala	Val	Lys 150	Asn	Phe	Val	Lys	Lys 155	Phe	Pro	His	Arg	Met 160	
Gly	Glu	Trp	Ser	Ala 165	Asp	Ser	Lys	Thr	Asn 170	Val	Ala	Thr	Met	Asp 175	Ala	
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Glu	Val	Gln 195	Ile	Lys	His	Ile	Ala 200	Ala	Asp	Gly	Thr	Glu 205	Thr	Ile	Leu	

Lys	Asp 210	Ser	Leu	Lys	Leu	Leu 215	Glu	Gly	Glu	Val	Leu 220	Asp	Gly	Thr	Val
Leu 225	Ser	Ala	Lys	Ala	Leu 230	Asp	Ala	Phe	Leu	Leu 235	Glu	Gln	Val	Ala	Arg 240
Ala	Lys	Ala	Glu	Gly 245	Ile	Leu	Phe	Ser	Ala 250	His	Leu	Lys	Ala	Thr 255	Met
Met	Lys	Val	Ser 260	Asp	Pro	Ile	Ile	Phe 265	Gly	His	Val	Val	Arg 270	Ala	Tyr
Phe	Ala	Asp 275	Val	Phe	Ala	Gln	Tyr 280	Gly	Glu	Gln	Leu	Leu 285	Ala	Ala	Gly
Leu	Asn 290	Gly	Glu	Asn	Gly	Leu 295	Ala	Ala	Ile	Leu	Ser 300	Gly	Leu	Glu	Ser
Leu 305	Asp	Asn	Gly	Glu	Glu 310	Ile	Lys	Ala	Ala	Phe 315	Glu	Lys	Gly	Leu	Glu 320
Asp	Gly	Pro	Asp	Leu 325	Ala	Met	Val	Asn	Ser 330	Ala	Arg	Gly	Ile	Thr 335	Asn
Leu	His	Val	Pro 340	Ser	Asp	Val	Ile	Val 345	Asp	Ala	Ser	Met	Pro 350	Ala	Met
Ile	Arg	Thr 355	Ser	Gly	His	Met	Trp 360	Asn	Lys	Asp	Asp	Gln 365		Gln	Asp
Thr	Leu 370	Ala	Ile	Ile	Pro	Asp 375	Ser	Ser	Tyr	Ala	Gly 380	Val	Tyr	Gln	Thr
Val 385	Ile	Glu	Asp	Cys	Arg 390	Lys	Asn	Gly	Ala	Phe 395	Asp	Pro	Thr	Thr	Met 400
Gly	Thr	Val	Pro	Asn 405	Val	Gly	Leu	Met	Ala 410	Gln	Lys	Ala	Glu	Glu 415	Tyr
Gly	Ser	His	Asp 420	Lys	Thr	Phe	Arg	Ile 425	Glu	Ala	Asp	Gly	Val 430	Val	Gln
Val	Val	Ser 435	Ser	Asn	Gly	Asp	Val 440	Leu	Ile	Glu	His	Asp 445	Val	Glu	Ala
Asn	Asp 450	Ile	Trp	Arg	Ala	Cys 455	Gln	Val	Lys	Asp	Ala 460	Pro	Ile	Gln	Asp
Trp 465	Val	Lys	Leu	Ala	Val 470	Thr	Arg	Ser	Arg	Leu 475	Ser	Gly	Met	Pro	Ala 480
Val	Phe	Trp	Leu	Asp 485	Pro	Glu	Arg	Ala	His 490	Asp	Arg	Asn	Leu	Ala 495	Ser
Leu	Val	Glu	Lys 500	Tyr	Leu	Ala	Asp	His 505	Asp	Thr	Glu	Gly	Leu 510	Asp	Ile
Gln	Ile	Leu 515	Ser	Pro	Val	Glu	Ala 520	Thr	Gln	Leu	Ser	Ile 525	Asp	Arg	Ile
Arg	Arg	Gly	Glu	Asp	Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp

540 535 530 Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys 550 Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu 630 635 Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu 665 Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn 680 Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys <210> 551 <211> 1059 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1059) <223> FRXA00521

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			gct Ala													192	
ctg Leu 65	aag Lys	gcc Ala	acc Thr	atg Met	atg Met 70	aag Lys	gtc Val	tcc Ser	gac Asp	cca Pro 75	atc Ile	atc Ile	ttc Phe	ggc Gly	cac His 80	240	
			gct Ala													288	
			gct Ala 100													336	
			gag Glu													384	
			ttg Leu													432	
Arg 145	Gly	Ile	acc Thr	Asn	Leu 150	His	Val	Pro	Ser	Asp 155	Val	Ile	Val	Asp	Ala 160	480	
			gca Ala													528	
Ásp	Glń	Ğlū	cag Gln 180	Āsp	Thr	Leu	Ála	Ile 185	Ile	Pro	Asp	Ser	Ser 190	Tyr	Āla	576	
Gly	Val	Tyr 195		Thr	Val	Ile	Glu 200	Āsp	Cys	Arg	Lys	Asn 205	Gly	Ala	Phe	624	
Asp	Pro 210	Thr	acc Thr	Met	Gly	Thr 215	Val	Pro	Asn	Val	Gly 220	Leu	Met	Ala	Gln	672	
Lys 225	Ala	Glu	gag Glu	Tyr	Gly 230	Ser	His	Asp	Lys	Thr 235	Phe	Arg	Ile	Glu	Ala 240	720	
Asp	Gly	Val	gtt Val	Gln 245	Val	Val	Ser	Ser	Asn 250	Gly	Asp	Val	Leu	Ile 255	Glu	768	
His	Asp	Val	gag Glu 260	Ala	Asn	Asp	Ile	Trp 265	Arg	Āla	Cys	Gln	Val 270	Lys	Asp	816	
gcc	cca	atc	cag	gat	tgg	gta	aag	ctt	gct	gtc	acc	cgc	tcc	cgt	ctc	864	

Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu 280 tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac 912 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp 295 960 cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr 310 315 1008 gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu 325 tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt 1056 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly 345 350 1059 aac Asn <210> 552 <211> 353 <212> PRT <213> Corynebacterium glutamicum <400> 552 Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln 85 Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe 115 Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala 135 Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala

Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp

145

155

170 175 165 Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala 185 Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala 230 Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp 265 Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu 280 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp 295 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr 310 315 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu 330 325 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn <210> 553 <211> 1694 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1671) <223> RXN02209 <400> 553 acc gag tcc acc gtt gtt cct tcc atc gct ggc cct aag cgc cca cag 48 Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln gac cgc atc ctt ctc tcc gag gca aag gag cag ttc cgt aag gat ctg Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu 20

cca acc tac acc gac gac gct gtt tcc gta gac acc tcc atc cct gca Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala

35

							ggc Gly									192
							tgg Trp									240
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							gac Asp									336
							tct Ser 120									384
							gca Ala									432
							cca Pro									480
							aag Lys									528
							acc Thr									576
							atc Ile 200									624
		Leu	Ser	Gly	Asn	Arg	aac Asn	Phe	Glu	Gly	Arg	Ile				672
							tcc Ser									720
							gac Asp									768
							ttc Phe									816
							cag Gln 280									864

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				gca Ala 325												1008
gca Ala	gtc Val	acc Thr	gac Asp 340	atc Ile	cag Gln	ggc Gly	gca Ala	cgc Arg 345	gtt Val	ctg Leu	gct Ala	aag Lys	ctc Leu 350	ggc Gly	gac Asp	1056
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				cgc Arg	_			-			_					1296
				tcc Ser												1344
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_	_			aac Asn	_				_	•	_					1440
				cac His 485												1488
				gca Ala												1536
	-			gac Asp				_		-						1584
act	cct	aag	act	gtc	aag	gtc	acc	gca	acc	aag	gag	aac	ggc	gac	gtc	1632

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Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
50 55 60

Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala 65 70 75 80

Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro 85 90 95

Gln Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser 100 105 110

Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro 130 135 140

Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr 145 150 155 160

Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr 165 170 175

Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu 180 185 190

Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr 195 200 205

Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp 210 215 220

Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala 225 230 235 240

Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly 360 Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp 375 Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg 390 395 Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala 405 410 Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser 475 Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly 505 Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu 515 Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val 535 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg 545 550

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atg gac Met Asp														768
aac gac Asn Asp		e Leu												816
gac acc Asp Thr														864
gca gat Ala Asp 290														912
acc ggt Thr Gly 305														960
gca cct Ala Pro														1008
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tcc gtc Ser Val														1344

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cac cgc tcc His Arg Ser											1488
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gac atc acc Asp Ile Thr 515		-							_		1584
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Ser	Ala	Ala 195	Ile	Asn	Glu	His	Asp 200	Leu	Thr	Ala	Thr	Ala 205	Val	Leu	Ser
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55

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr 200 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile 215 220 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro 235 230 Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr 250 Ala Thr <210> 559 <211> 817 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(817) <223> FRXA02213 <400> 559 ttctgtggaa tgagaatccg atgtttttct cacgccggct cagccgaagc agacgccgtc 60 gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag Val Thr Glu Ser Lys 163 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr 10 15

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	c cca n Pro															499
	c cgc y Arg 135															547
	c gag n Glu 0															595
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	t gag e Glu														Tyr	691
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	aac Asn															336
	tac Tyr															384
	gtt Val 130															432
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				ggc Gly 565												1728
				gct Ala												1776
Pro	Arg	Val 595	Āla	ccc Pro	Val	Āla	Lys 600	Lys	Arg	Val	Ser	Ser 605	Val	Thr	Glu	1824
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	_		-	gtc Val				-	_		-		-		-	2064
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atg act of Met Thr 1													2352
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ttc act o													2496
gca gat d Ala Asp													2544
tac tac Tyr Tyr 850													2592
gcg atc Ala Ile 865			u Met										2640
tcc gag (Ser Glu													2688
cag gat													2736
ctc cca Leu Pro													2784
cgc gct Arg Ala 930													2832
gag gag Glu Glu 945			e Asp						taaq	gtcti	ta		2878 [.]
tagtcctg	ca cta												2891

<210> 562 <211> 956 <212> PRT

<213> Corynebacterium glutamicum

<400> 562

Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly 1 5 10 15

Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp 20 ,25 30

Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr 35 40 45

Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg 50 55 60

Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe 65 70 75 80

Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val 85 90 95

Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu 100 105 110

Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser 115 120 125

Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile 130 135 . 140

Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val 145 150 155 160

Gly Gly Phe Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser 165 170 175

Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His 180 185 190

Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala 195 200 205

Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys 210 215 220

Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val 225 230 235 240

Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu 245 250 255

Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val260 265 270

Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile 275 280 285

Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met 290 295 300

Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly

305	310		3:	15	32	20
Ser Glu Gly G	Sln His Leu 325	Gln Met	Phe Gly A: 330	sp Gly Glu	Ile Lys Va 335	al
Ser Leu Thr A	Ala Asn Pro 340		Leu Glu A 345	la Val Asn	Pro Ala Me 350	et
Glu Gly Ile V 355	al Arg Ala	Lys Gln 3	Asp Tyr L	eu Asp Lys 365	Gly Val As	sp
Gly Lys Thr V 370	Val Val Pro	Leu Leu 3 375	Leu His G	ly Asp Ala 380	Ala Phe Al	la
Gly Leu Gly I 385	le Val Pro 390	Glu Thr		eu Ala Lys 95		ly 00
Tyr Asp Val G	Gly Gly Thr 405	Ile His	Ile Val V 410	al Asn Asn	Gln Ile GI 415	ly
Phe Thr Thr T	Thr Pro Asp 120		Arg Ser M 425	et His Tyr	Ala Thr As 430	sp
Tyr Ala Lys A 435	Ala Phe Gly	Cys Pro	Val Phe H	is Val Asn 445	Gly Asp As	sp
Pro Glu Ala V 450	/al Val Trp	Val Gly 455	Gln Leu A	la Thr Glu 460	Tyr Arg Aı	rg
Arg Phe Gly L 465	Lys Asp Val 470	Phe Ile		al Cys Tyr 75		rg 80
Gly His Asn G	Glu Ala Asp 485	Asp Pro	Ser Met T	hr Gln Pro	Lys Met Ty 495	yr
Glu Leu Ile T 5	Thr Gly Arg		Val Arg A 505	la Gln Tyr	Thr Glu As 510	sp
Leu Leu Gly A 515	Arg Gly Asp	Leu Ser . 520	Asn Glu A	sp Ala Glu 525	Ala Val Va	al
Arg Asp Phe H 530	His Asp Gln	Met Glu 535	Ser Val P	he Asn Glu 540	Val Lys Gl	lu
Gly Gly Lys L 545	Lys Gln Ala 550	Glu Ala		ly Ile Thr 55		1n 60
Lys Leu Pro H	His Gly Leu 565	Glu Thr .	Asn Ile So 570	er Arg Glu	Glu Leu Le 575	eu
Glu Leu Gly G 5	Gln Ala Phe 580		Thr Pro G 585	lu Gly Phe	Asn Tyr Hi 590	is
Pro Arg Val A 595	Ala Pro Val	Ala Lys 600	Lys Arg V	al Ser Ser 605	Val Thr Gl	lu
Gly Gly Ile A	Asp Trp Ala	Trp Gly 615	Glu Leu L	eu Ala Phe 620	Gly Ser Le	eu
Ala Asn Ser G 625	Gly Arg Leu 630	Val Arg		ly Glu Asp 35		rg 40

Gly	Thr	Phe	Thr	Gln 645	Arg	His	Ala	Val	Ala 650	Ile	Asp	Pro	Ala	Thr 655	Ala
Glu	Glu	Phe	Asn 660	Pro	Leu	His	Glu	Leu 665	Ala	Gln	Ser	Lys	Gly 670	Asn	Asn
Gly	Lys	Phe 675	Leu	Val	Tyr	Asn	Ser 680	Ala	Leu	Thr	Glu	Tyr 685	Ala	Gly	Met
Gly	Phe 690	Glu	Tyr	Gly	Tyr	Ser 695	Val	Gly	Asn	Glu	Asp 700	Ser	Ile	Val	Ala
Trp 705	Glu	Ala	Gln	Phe	Gly 710	Asp	Phe	Ala	Asn	Gly 715	Ala	Gln	Thr	Ile	Ile 720
Asp	Glu	Tyr	Val	Ser 725	Ser	Gly	Glu	Ala	Lys 730	Trp	Gly	Gln	Thr	Ser 735	Lys
Leu	Ile	Leu	Leu 740	Leu	Pro	His	Gly	Tyr 745	Glu	Gly	Gln	Gly	Pro 750	Asp	His
Ser	Ser	Ala 755	Arg	Ile	Glu	Arg	Phe 760	Leu	Gln	Leu	Cys	Ala 765	Glu	Gly	Ser
Met	Thr 770	Val	Ala	Gln	Pro	Ser 775	Thr	Pro	Ala	Asn	His 780	Phe	His	Leu	Leu
Arg 785	Arg	His	Ala	Leu	Ser 790	Asp	Leu	Lys	Arg	Pro 795		Val	Ile	Phe	Thr 800
Pro	Lys	Ser	Met	Leu 805	Arg	Asn	Lys	Ala	Ala 810	Ala	Ser	Ala	Pro	Glu 815	Asp
Phe	Thr	Glu	Val 820	Thr	Lys	Phe	Gln	Ser 825	Val	Ile	Asn	Asp	Pro 830	Asn	Val
Ala	Asp	Ala 835	Ala	Lys	Val	Lys	Lys 840	Val	Met	Leu	Val	Ser 845	Gly	Lys	Leu
Tyr	Tyr 850	Glu	Leu	Ala	Lys	Arg 855	Lys	Glu	Lys	Asp	Gly 860	Arg	Asp	Asp	Ile
Ala 865	Ile	Val	Arg	Ile	Glu 870	Met	Leu	His	Pro	Ile 875	Pro	Phe	Asn	Arg	Ile 880
Ser	Glu	Ala	Leu	Ala 885	Gly	Tyr	Pro	Asn	Ala 890	Glu	Glu	Val	Leu	Phe 895	Val
Gln	Asp	Glu	Pro 900	Ala	Asn	Gln	Gly	Pro 905	Trp	Pro	Phe	Tyr	Gln 910	Glu	His
Leu	Pro	Glu 915	Leu	Ile	Pro	Asn	Met 920	Pro	Lys	Met	Arg	Arg 925	Val	Ser	Arg
Arg	Ala 930	Gln	Ser	Ser	Thr	Ala 935	Thr	Gly	Val	Ala	Lys 940	Val	His	Gln	Leu
Glu 945	Glu	Lys	Gln	Leu	Ile 950	Asp	Glu	Ala	Phe	Glu 955	Ala				

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Val	Pro	Tyr 195	Val	Thr	Pro	Leu	Val 200	Arg	Lys	Leu	Ala	Glu 205	Lys	His	Gly	
						acc Thr 215										672
						gct Ala										720
-	_	_		-		gct Ala				_		-	-			768
aag Lys	gct Ala	aag Lys	ctc Leu 260	cgt Arg	ggt Gly	acc Thr	act Thr	cag Gln 265	aag Lys	gtc Val	aac Asn	cgc Arg	atc Ile 270	cgt Arg	gag Glu	816
			-	_		gtc Val		_	_	_			_			864
						gat Asp 295										912
_		-				atc Ile		_								960
_					_	gca Ala	-	-		-	_	-				1008
	-					aac Asn		-		_		-				1056
						atc Ile										1104
						gct Ala 375										1152
_	-		-	_	_	gct Ala	-	_		-			_	_	-	1200
						ggc Gly										1248
						acc Thr										1296
						atc Ile										1344

440 445 435 gat gga att gat too ato gog ato ogt cag atg gto tto ota coa otg 1392 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu 450 455 460 acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg 1440 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu 465 470 475 acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg 1488 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu 495 485 490 1517 cag ctc taagatctct gcaagttaaa acc Gln Leu

<210> 564

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

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Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Ala 20 25 30

Ala Pro Ala Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
35 40 '45

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu 50 55 60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp 65 70 75 80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Glu 85 90 95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly 100 105 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
115 120 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala 130 135 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Pro Val Lys Glu Glu 145 150 155 160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala 165 170 175

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn 180 185 190

Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly 200 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg 215 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu 230 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro 330 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu 360 Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly 425 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu 440 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu 455 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu 470 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu

Gln Leu

485

490

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ggc ggt gac cca Gly Gly Asp Pro 185					691
ttt gaa gct gat Phe Glu Ala Asp 200					739
ggt gga gat gca Gly Gly Asp Ala 215					787 ⁻
aca aaa cca gtt Thr Lys Pro Val 230					835
aag acc atg ggg Lys Thr Met Gly					883
gcg cga gca aag Ala Arg Ala Lys 265	Lys His Ala				931
aca act ccg agt Thr Thr Pro Ser 280					979
ttg taactaacag Leu	gccacagatc t	ta			1005
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Thr Gly Ser Glu 20		His Ala Arg 25	Arg Ile Leu	Ala Ser Gly 30	
Ala Lys Leu Val 35	Gly Gly Thr	Asn Pro Arg 40	Lys Ala Gly 45	Gln Thr Ile	
Leu Ile Asn Asp 50	Thr Glu Leu 55	Pro Val Phe	Gly Thr Val	Lys Glu Ala	
Met Glu Glu Thr 65	Gly Ala Asp 70	Val Thr Val	Ile Phe Val	Pro Pro Ala 80	

Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu

90

120 125 115 Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val 200 Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp, Phe Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe 230 235 Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala Leu 290 <210> 567 <211> 1395 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1372) <223> RXA00783 <400> 567 aaagttccca aggggtgggg gctgagcacc acggatccaa ttttgttgca atttgcaaag 60 tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt Leu Lys His Leu Leu tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro 15 gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211

Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu 25 30 35

ttt Phe	gaa Glu	acc Thr 40	cat His	ggt Gly	gtg Val	cca Pro	gtg Val 45	ttg Leu	aag Lys	gga Gly	att Ile	gtg Val 50	gca Ala	tca Ser	aca Thr	259
cca Pro	gag Glu 55	gcg Ala	gcg Ala	agg Arg	aaa Lys	gcg Ala 60	gct Ala	gag Glu	gaa Glu	atc Ile	ggc Gly 65	gga Gly	ctg Leu	acc Thr	gtc Val	307
						gtg Val										355
						gct Ala										403
						gga Gly										451
						gag Glu										499
						ctg Leu 140										547
						aag Lys										595
						ggt Gly										643
-		-	-			gaa Glu				-			-		_	691
						cag Gln										739
_				_	-	gtg Val 220		_	_	-		_				787
						ctg Leu										835
						gaa Glu										883
						gat Asp										931
gtg	ggc	atc	att	ggc	aat	ggt	gca	ggt	ttg	gtg	atg	tcc	acg	ttg	gat	979

Val	Gly	Ile 280	Ile	Gly	Asn	Gly	Ala 285	Gly	Leu	Val	Met	Ser 290	Thr	Leu	Asp	
atc Ile	gtg Val 295	gct Ala	gca Ala	gct Ala	ggt Gly	gaa Glu 300	cgc Arg	cat His	ggt Gly	ggg Gly	cag Gln 305	cgc Arg	ccc Pro	gcg Ala	aac Asn	1027
ttc Phe 310	cta Leu	gac Asp	att Ile	ggt Gly	ggc Gly 315	gga Gly	gca Ala	tca Ser	gct Ala	gaa Glu 320	tcg Ser	atg Met	gct Ala	gct Ala	ggt Gly 325	1075
	gat Asp															1123
	ttt Phe															1171
gga Gly	gct Ala	ttg Leu 360	gat Asp	gtg Val	ctc Leu	ggc Gly	gat Asp 365	caa Gln	gca Ala	acg Thr	aag Lys	cct Pro 370	ctt Leu	gtg Val	gtg Val	1219
	ctt Leu 375															1267
	aac Asn															1315
	cac His															1363
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Ser	Lys	His	Gly 20	Pro	Glu	Met	Glu	Leu 25	Ala	Val	Asp	Leu	Phe 30	Glu	Tyr	
Gln	Ala	Arg 35	Asp	Leu	Phe	Glu	Thr 40	His	Gly	Val	Pro	Val 45	Leu	Lys	Gly	
Ile	Val 50	Ala	Ser	Thr	Pro	Glu 55	Ala	Ala	Arg	Lys	Ala 60	Ala	Glu	Glu	Ile	
Gly 65	Gly	Leu	Thr	Val	Val 70	Lys	Ala	Gln	Val	Lys 75	Val	Gly	Gly	Arg	Gly 80	

Lys	Ala	Gly	Gly	Val 85	Arg	Val	Ala	Pro	Thr 90	Ser	Ala	Gln	Ala	Phe 95	Asp
Ala	Ala	Asp	Ala 100	Ile	Leu	Gly	Met	Asp 105	Ile	Lys	Gly	His	Thr 110	Val	Asn
Gln	Val	Met 115	Val	Ala	Gln	Gly	Ala 120	Asp	Ile	Ala	Glu	Glu 125	Tyr	Tyr	Phe
Ser	Ile 130	Leu	Leu	Asp	Arg	Ala 135	Asn	Arg	Ser	Tyr	Leu 140	Ala	Met	Cys	Ser
Val 145	Glu	Gly	Gly	Met	Glu 150	Ile	Glu	Ile	Leu	Ala 155	Lys	Glu	Lys	Pro	Glu 160
Ala	Leu	Ala	Lys	Val 165	Glu	Val	Asp	Pro	Leu 170	Thr	Gly	Ile	Asp	Glu 175	Asp
Lys	Ala	Arg	Glu 180	Ile	Val	Thr	Ala	Ala 185	Gly	Phe	Glu	Thr	Glu 190	Val	Ala
Glu	Lys	Val 195	Ile	Pro	Val	Leu	Ile 200	Lys	Ile	Trp	Gln	Val 205	Tyr	Tyr	Glu
Glu	Glu 210	Ala	Thr	Leu	Val	Glu 215	Val	Asn	Pro	Leu	Val 220	Leu	Thr	Asp	Asp
Gly 225	Asp	Val	Ile	Ala	Leu 230	Asp	Gly	Lys	Ile	Thr 235	Leu	Asp	Asp	Asn	Ala 240
Asp	Phe	Arg	His	Asp 245	Asn	Arg	Gly	Ala	Leu 250	Ala	Glu	Ser	Ala	Gly 255	Gly
Leu	Asp	Ile	Leu 260	Glu	Leu	Lys	Ala	Lys 265	Lys	Asn	Asp	Leu	Asn 270	Tyr	Val
Lys	Leu	Asp 275	Gly	Ser	Val	Gly	Ile 280	Ile	Gly	Asn	Gly	Ala 285	Gly	Leu	Val
Met	Ser 290	Thr	Leu	Asp	Ile	Val 295	Ala	Ala	Ala	Gly	Glu 300	Arg	His	Gly	Gly
Gln 305	Arg	Pro	Ala	Asn	Phe 310	Leu	Asp	Ile	Gly	Gly 315	Gly	Ala	Ser	Ala	Glu 320
Ser	Met	Ala	Ala	Gly 325	Leu	Asp	Val	Ile	Leu 330	Gly	Asp	Ser	Gln	Val 335	Arg
Ser	Val	Phe	Val 340	Asn	Val	Phe	Gly	Gly 345	Ile	Thr	Ala	Cys	Asp 350	Val	Val
Ala	Lys	Gly 355	Ile	Val	Gly	Ala	Leu 360	Asp	Val	Leu	Gly	Asp 365	Gln	Ala	Thr
Lys	Pro 370	Leu	Val	Val	Arg	Leu 375	Asp	Gly	Asn	Asn	Val 380	Val	Glu	Gly	Arg
Arg 385	Ile	Leu	Ala	Glu	Tyr 390	Asn	His	Pro	Leu	Val 395	Thr	Val	Val	Glu	Gly 400
Met	Asp	Ala	Ala	Ala	Asp	His	Ala	Ala	His	Leu	Ala	Asn	Leu	Ala	Gln

405 410 415

His Gly Gln Phe Ala Thr Ala Asn 420

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595

gge atg ace tae get gae gat gaa get ace tte ace gag aag etg eet

Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro

150	155	160	165
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		gct cag acc aag cag Ala Gln Thr Lys Gln 195	
		atc cgc tat ggc cac Ile Arg Tyr Gly His 210	
		tgg atc gtg acc gtc Trp Ile Val Thr Val 225	
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	Tyr Ala Leu Asp Leu	ctt cgc agc gca ggc Leu Arg Ser Ala Gly 260	
		gta tcc ggc ctg tgg Val Ser Gly Leu Trp 275	
		g cac gca gcc aag gta His Ala Ala Lys Val 290	
		tct gtt cct cac ctt Ser Val Pro His Leu 305	
		ctc ttt gga cct tac Leu Phe Gly Pro Tyr 320	
	Phe Leu Lys Glu Gly	tcc tac ctg gac ctg Ser Tyr Leu Asp Leu 340	
		tac ctt ggc gtt gct Tyr Leu Gly Val Ala 355	
		act gaa gtt ctc aag Thr Glu Val Leu Lys 370	
		tac atg cca gag gca Tyr Met Pro Glu Ala 385	
		cag cgt gtt cag gtt Gln Arg Val Gln Val 400	

aag cct gca Lys Pro Ala											1363
ttg atc aac Leu Ile Asn			Thr I								1411
cct gga gca Pro Gly Ala 440		-	_	_			_			_	1459
tgc ttc ggt Cys Phe Gly 455					Asp						1507
atc cct tcc Ile Pro Ser 470											1555
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145

140

135

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	_	-			gac Asp					_	-		_	_		691
_	-	_	-	-	gtt Val	-			-		-				_	739
-	_	-		_	gct Ala	-		-	-					_	-	787
	-				gac Asp 235		-			_	-					835
					tac Tyr											883
					ttc Phe											931
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	cgc Arg	-														1039
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Val	Val	Leu	Ile 20	Gly	Ala	Gly	Ile	Met 25	Ser	Ser	Thr	Leu	Gly 30	Ala	Met	
Leu	Arg	Gln 35	Leu	Glu	Pro	Ser	Trp 40	Thr	Gln	Ile	Val	Phe 45	Glu	Arg	Leu	

Asp Gly Pro Ala Gln Glu Ser Ser Pro Trp Asn Asn Ala Gly Thr 50 55 60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly 65 70 75 80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val 85 90 95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp 100 105 110

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly 115 120 125

Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp 130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe 145 150150155160

Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro 165 170 175

Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala 180 185 190

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile 195 200 205

Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp 210 215 220

Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys 225 230 235 240

Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu 245 250 255

Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val 260 265 270

Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His 275 280 285

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Val Pro His Leu Asp Thr Arg Val Ile 305 310

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Gly	Asp	Lys 35	Leu	Lys	Asp	Met	Ile 40	Pro	Ser	Tyr	Gly	Lys 45	Lys	Leu	Ala	
Ser	Glu 50	Pro	Ala	Leu	Phe	Glu 55	Gln	Gln	Trp	Ala	Arg 60	Thr	Gln	Lys	Thr	
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gago	ette	ecg (caaaa	aacad	ec ga	nttaa	ıcaaç	g gct	:aaat	gat				gac Asp		115

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													cgc Arg 35			211
													gtt Val			259
													ggc Gly			307
													ggc Gly			355
													aag Lys			403
_		-			-		_	_	_				gtt Val 115	_	-	451
													atc Ile			499
													cgt Arg			547
													gtt Val			595
		Gln		Gly	Thr		Val	Val	Ile	Leu	Ala	Ala	ctg Leu			643
													att Ile 195			691
tcc Ser	ggc Gly	gca Ala 200	ggc Gly	gca Ala	gcg Ala	ggc Gly	gtt Val 205	gca Ala	gct Ala	gta Val	gat Asp	atg Met 210	ctg Leu	acc Thr	aac Asn	739
													atc Ile			7 87
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acc aac cct cqt qqc atc aqc qqt qqc atc aat gag gct ttc acc ggc 883 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly 250 255 gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala 265 270 ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro 280 285 acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val 305 295 300 gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser 315 <210> 576 <211> 321 <212> PRT <213> Corynebacterium glutamicum Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu 10 Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg 25 . Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val 40 Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 105 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 120 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser 130 135 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 150 155 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp

185 190 180 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Gly Val Ala Ala Val 200 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 215 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 230 235 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser <210> 577 <211> 1347 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1324) <223> RXN01048 <400> 577 agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60 gagetteecg caaaaacace gattaacaag getaaatgat atg ace ate gae etg Met Thr Ile Asp Leu cag cgt tee ace caa aac ete ace cat gag gaa ate tte gag gea cae 163 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His 10 15 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met 30 259 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu 45 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly

55 60 65

					att Ile 75											355
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					gct Ala											451
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					acc Thr											643
					gat Asp											691
					gcg Ala											739
					atc Ile											787
					ctt Leu 235											835
					atc Ile											883
	-	_			ggc Gly									-	_	931
			_	-	ccg Pro				_			_				979
					cct Pro											1027

									aac Asn					1075
									aag Lys					1123
									tcg Ser					1171
_		_		_	-	•	_	-	ccg Pro					1219
	_		_			_	_		 ccg Pro 385	_		-	_	1267
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<400> 578

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Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser

130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys . 290 295 300

Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile 305 310 315 320

Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala 325 330 335

Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln 340 345 350

Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu 355 360 365

Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg 370 375 380

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Leu Pro Val Glu Ala Pro Ile Phe 405

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tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro 50 55 60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu 65 70 75 80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
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95

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<400> 580

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Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr 35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro 50 55 60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu 65 70 75 80

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tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile 691

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Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 115 120 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser 135 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 150 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 230 235 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 265 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 280 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 295 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser <210> 583 <211> 582 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(582) <223> RXN03101 <400> 583 48 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala 10

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40

35

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act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc ac Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Th 70 75 80 8	r
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Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gl 50 55 60	у
Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Th. 65 70 75 8	
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Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Th 100 105 110	r
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691

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185 190 195

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					aac Asn											931
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					acc Thr											1219
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Asn Ala Ser	Leu Asn							
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Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln 100 105 110	
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Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn 130 135 140	
Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser 145 150 155 160	
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			atc acc tct Ile Thr Ser 240		
			cgc acc gca Arg Thr Ala 255		
			atc gca cgt Ile Ala Arg		
	Ala Asp Met		gag acc ggc Glu Thr Gly		
			gtt cgc tct Val Arg Ser 305		
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			cag aag gaa Gln Lys Glu 335		
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	Phe Asp Leu		tac gct cgc Tyr Ala Arg		
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			gag gtt ggc Glu Val Gly 400		
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35 40 45

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly 50 55 60

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val 65 70 75 80

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln 85 90 95

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser 100 105 110

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn 115 120 125

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser 130 135 140

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe 145 150 155 160

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala 165 170 175

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys 180 185 190

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile 195 200 205

Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro 210 - 215 220

Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr 225 230 235 240

Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr 245 250 255

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala 260 265 270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr 275 280 285

Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg 290 295 300

Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe 310 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala 360 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val 390 Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn 425 <210> 593 <211> 2340 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2317) <223> RXN02404 <400> 593 gttttcacaa ccgttaacgg cgtagccaaa caagaaggat tcgcattctt ctggtttagg 60 115 cacaggtcat ctaaaaccca tgctttaaaa ggagccttca atg act gaa cag gaa Met Thr Glu Gln Glu 1 ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa 163 Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu 10 1.5 cgc gtt gac gcg ggc gga atg cag gtt gca aaa gtt ctc tac gac ttt 211 Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe gta acc gaa gcg gta ctc cct cgc gtg ggt gtg gat gcg gaa aag ttc 259 Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe 45

307

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Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg

60

gag Glu 70	ctg Leu	ctt Leu	gct Ala	cgc Arg	cgc Arg 75	gat Asp	gaa Glu	ctg Leu	cag Gln	atg Met 80	ctt Leu	atc Ile	gac Asp	gac Asp	tac Tyr 85	355
cac His	cgc Arg	aac Asn	aac Asn	tcc Ser 90	ggc Gly	acc Thr	atc Ile	gac Asp	caa Gln 95	gag Glu	gcg Ala	tac Tyr	gag Glu	gat Asp 100	ttc Phe	403
					tac Tyr											451
					gat Asp											499
					ctg Leu											547
					ctc Leu 155											595
cca Pro	gaa Glu	act Thr	gat Asp	ggc Gly 170	gct Ala	gaa Glu	aag Lys	ggc Gly	aag Lys 175	gag Glu	tac Tyr	aac Asn	ccg Pro	gtc Val 180	cgc Arg	643
ggc Gly	cag Gln	aag Lys	gtc Val 185	atc Ile	gag Glu	tgg Trp	ggt Gly	cgt Arg 190	gaa Glu	ttc Phe	ctc Leu	gac Asp	agc Ser 195	gtt Val	gtc Val	691
cca Pro	ctg Leu	gac Asp 200	ggt Gly	gct Ala	tcg Ser	cat His	gcc Ala 205	gat Asp	gtt Val	gag Glu	aag Lys	tac Tyr 210	aac Asn	atc Ile	acc Thr	739
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					cgt Arg 235											835
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					ggc Gly											931
gtt Val	ttg Leu	gaa Glu 280	tct Ser	gcg Ala	atc Ile	acc Thr	acg Thr 285	atc Ile	atg Met	gac Asp	ttc Phe	gaa Glu 290	gac Asp	tcc Ser	gtt Val	979
gca Ala	gct Ala 295	gtt Val	gat Asp	gct Ala	gaa Glu	gac Asp 300	aag Lys	acc Thr	tta Leu	ggt Gly	tac Tyr 305	tct Ser	aac Asn	tgg Trp	ttc Phe	1027
gga	ctc	aac	acc	ggc	gaa	ctg	aaa	gaa	gag	atg	tcc	aag	aac	gga	cgc	1075

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					caa Gln											1219
					atg Met											1267
					cag Gln 395											1315
					cct Pro											1363
					ggc Gly											1411
					ggt Gly										gtg Val	1459
					atc Ile											1507
				-	gac Asp 475	_			-	_					_	1555
gaa Glu	gca Ala	ggc Gly	gcc Ala	atg Met 490	gtg Val	cgc Arg	aag Lys	gct Ala	gat Asp 495	atg Met	cag Gln	acc Thr	gca Ala	ccg Pro 500	tgg Trp	1603
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					cag Gln											1699
					ctg Leu											1747
					gtt Val											1795

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	gac agc ctg cgc aac Asp Ser Leu Arg Asn 590									
	tgg tct gag gaa gag Trp Ser Glu Glu Glu 605									
	atc ctc gga tac gtt Ile Leu Gly Tyr Val 620									
	aag gtt cca gac atc Lys Val Pro Asp Ile 635									
	ctg cgt att tcc tcg Leu Arg Ile Ser Ser 655									
	gtc tcg aag gag cag Val Ser Lys Glu Gln 670		_							
	gtc gac aag caa aat Val Asp Lys Gln Asn 685									
	aag tac gac gcc tcc Lys Tyr Asp Ala Ser 700									
2 2	gaa ggc acc aag tcc Glu Gly Thr Lys Ser 715	2 22	• •							
ccc atc ttg cac gca Pro Ile Leu His Ala 730	cgc cgc cgc gag ttc Arg Arg Arg Glu Phe 735	aaa gca aaa aac Lys Ala Lys Asn	2317							
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Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val 35 40 45

- Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu 50 60
- Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met 65 70 75 80
- Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu 85 90 95
- Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro 100 105 110
- Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser 115 120 125
- Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala 130 135 140
- Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr 145 150 155 160
- Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu 165 170 175
- Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe 180 185 190
- Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu
 195 200 205
- Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser 210 215 220
- Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn 225 230 235 240
- Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile 245 250 255
- Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr 260 265 270
- Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp 275 280 285
- Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly 290 295 300
- Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met 305 310 315
- Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val 325 330 335
- Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu 340 345 350
- Leu Phe Val Arg Asn Val Gly His Leu Met Gln Asn Pro Ser Ile Leu

355 360 365

Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met Asp Ala Val Leu Thr 370 380

Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn 385 395 400

Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro 405 410 415

Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly Arg Val Glu Asp Leu 420 425 430

Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly Val Met Asp Glu Glu
435 440 445

Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile Met Glu Val Ala Asp 450 455 460

Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu 465 470 475 480

Ile His Thr Ser Met Glu Ala Gly Ala Met Val Arg Lys Ala Asp Met 485 490 495

Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn Asn Asn Val Asp Ala 500 505 510

Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln Ile Gly Lys Gly Met 515 520 525

Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu Glu Lys Lys Ile Gly 530 535 540

Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly 545 550 555 560

Ala Thr Leu His Ala Thr His Tyr His Leu Val Asp Val Phe Lys Val 565 570 575

Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile 580 585 590

Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys
595 600 605

Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val 610 615 620

Arg Trp Val Glu His Gly Val Gly Cys Ser Lys Val Pro Asp Ile His 625 630 635 640

Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln 645 650 655

Met Leu Ala Asn Trp Ile Arg His Asp Val Val Ser Lys Glu Gln Val 660 665 670

Leu Glu Ser Leu Glu Arg Met Ala Val Val Asp Lys Gln Asn Ala 675 680 685

Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu 695 690 Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg Arg Glu Phe Lys 730 Ala Lys Asn <210> 595 <211> 2159 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(2136) <223> FRXA02404 <400> 595 atg cag gtt gca aaa gtt ctc tac gac ttt gta acc gaa gcg gta ctc 48 Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu 96 cct cgc gtg ggt gtg gat gcg gaa aag ttc tgg tcc gga ttc gcc gcc Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala 144 ate gee egg gae etc ace cea ege aac ege gag etg ett get ege ege Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg 192 gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly 55 acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac 240 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr 70 ttg gtt gag gag cca gaa gct gca gaa atc cgt acc caa aac gtc gat 288 Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp 85 90 336 acg gaa atc tcc agc acc gca gga cct cag ctg gtt gtt cca att ctg Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu 100 105 aac gca cgc ttc gcg ctg aac gct gcc aat gct cgc tgg ggt tcc ctc 384 Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu 120 432 tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala 135

-	_		aag Lys				_	_	_		_	-	_			480
		-	gaa Glu			•	-	•	-		_	-		_	_	528
			gtt Val 180													576
			gat Asp	-	-		_	_			_	-			-	624
			ggc Gly													672
		_	cac His			_	_		-		_					720
			aag Lys													768
	_		atg Met 260	-		-	-		_	-	_	-	-	-	_	816
			tta Leu													864
-		-	gag Glu	-		-			-				-			912
			cgc Arg	Val		Ile			Asn		Thr					960
			tcc Ser													1008
			atc Ile 340	-		-						-			_	1056
			ttg Leu													1104
			cgc Arg													1152
aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	acc	aac	gag	ctc	ttc	ggc	1200

Lys 0	Sln	His	Gly	Pro	Glu 390	Glu	Val	Ala	Phe	Thr 395	Asn	Glu	Leu	Phe	Gly 400	
cgc g Arg V	-		_	_		_	_		-			_	_	_		1248
gtt a Val M																1296
atg g Met G																1344
cgc a Arg T																1392
cgc a Arg I 465																1440
aac a Asn A																1488
atc o																1536
gag a Glu I																1584
cct t Pro S																1632
gat ç Asp V 545			_	-		_	-	_	-	_	_		_	-	-	1680
agc c Ser I	_	_								-						1728
tct g Ser G	_	-		_	_	_		_	_			_	-			1776
ctc g Leu G																1824
gtt c Val F																1872
cgt a Arg I																1920

635 640 625 630 tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc · Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val 645 650 gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa 2064 Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu 680 675 ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc 2112 Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg 695 700 cgc cgc gag ttc aaa gca aaa aac taagcacgct tttcgacgct tac 2159 Arg Arg Glu Phe Lys Ala Lys Asn 705 710 <210> 596 <211> 712 <212> PRT <213> Corynebacterium glutamicum <400> 596 Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly 55 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp 90 Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu 100 105 Asn Ala Arg Phe Ala Leu Asn Ala Asn Ala Arg Trp Gly Ser Leu 120 Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala 130 135 Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu 150 Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser 170 165

His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala 185 His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg 200 Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr 215 Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly 230 235 Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln 330 Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly 395 Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile 425 Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp 435 440 Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val 455 Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn 470 Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln 485 490

Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu 505 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val 520 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp 545 550 555 560 Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp 570 Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile 585 Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys 600 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu 615 Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu 680 Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg 695 Arg Arg Glu Phe Lys Ala Lys Asn 705 <210> 597 <211> 873 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(850) <223> RXA01089 <400> 597 aaaaattcgg ttcacaaaag gtttatcagt ccagcttaaa cccatcgcac gggcgggaga 60 attagactca aggcacatca cattgaagga gcttcttatc ttg tct cga ttt gct Leu Ser Arg Phe Ala qcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163

Ala	Asn	Leu	Ser	Leu 10	Thr	Phe	Thr	Glu	Leu 15	Asp	Phe	Leu	Asp	Arg 20	Phe	
gat (-	-	-	-		-		_	_				_			211
tac Tyr																259
ctg Leu																307
gcg Ala 70	-	_	-			_	_									355
atc Ile	-		_			_	•		_	-	_		-	_	_	403
ggc Gly			-	-			-		_		_					451
att Ile	-		-		_				_		-	_	-	_	-	499
att (547
tta Leu 150		_						_	•		-					595 ·
aag Lys				•					_	_						643
acc Thr																691
caa Gln																739
aat Asn	-								_	_	-			-		787
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Glu Phe Gln Tyr Pro Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg 35 40 45

Ala Asp Ser Ala Gly Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly 50 55 60

Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln 65 70 75 80

Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys 85 90 95

Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala 100 105 110

Arg Tyr Val Glu Asn Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu 115 120 125

Asp Val Val Val Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly
130 135 140

Tyr Phe Leu His Thr Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile 145 150 155 160

Ala His Pro Asn Val Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln 165 170 175

Ile His Gly Asn Leu Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly 180 185 190

Leu Leu Gly His Val Gln Val Ala Ser Val Pro Asp Arg His Glu Pro 195 200 205

Gly Thr Gly Glu Val Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu 210 215 220

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Thr Thr Ala Gly Leu Gly Trp Leu Glu Leu 245 250

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Met Thr Phe Lys Leu
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gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211 Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp

tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259 Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser 40 50

tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307 Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg 55 60 65

gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag 355 Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys 70 75 80 85

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gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc 451 Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu 105 110 115

tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca 499
Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala
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Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln
170 175 180

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Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu 65 70 75 80	
Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr 85 90 95	
Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr	
Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu 115 120 125	
Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu 130 135 140	
Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu 145 150 155 160	
Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp 165 170 175	
Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg 180 185 190	

Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly 195 200 Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp 225 230 235 Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe . 250 245 Thr Val <210> 601 <211> 1575 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (41)..(1552) <223> RXN03117 <400> 601 tgtgcaacat tagttcgtta agaagagtca cattccagcc atg att acc cac gaa Met Ile Thr His Glu 1 103 qtq cqc acc cac cqt tct qcq qaa qaq ttc ccq tac aag aag cac ctg Val Arq Thr His Arq Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu 10 151 gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala 25 gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg 199 Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val 40 cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met 55 gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt 295 Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly 70 ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act 343 Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr - 100 gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac 391 Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr 105 tee cae cca gga gat aac att eet eeg att ttg get gea gea eag eag 439

Ser	His	Pro 120	Gly	Asp	Asn	Ile	Pro 125	Pro	Ile	Leu	Ala	Ala 130	Ala	Gln	Gln	
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gag Glu 150	att Ile	cag Gln	gtt Val	aac Asn	ttg Leu 155	gtg Val	cgt Arg	gga Gly	atg Met	tgc Cys 160	ctg Leu	cat His	gag Glu	cac His	aag Lys 165	535
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				cgc Arg												775
				gac Asp 250												823
				att Ile												871
				tac Tyr												919
				ttg Leu												967
				cgt Arg												1015
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				tcg Ser												1111
ttc Phe	gct Ala	gtc Val	gcg Ala	ctg Leu	aag Lys	gat Asp	cgc Arg	gcg Ala	tgg Trp	cac His	cac His	gag Glu	cgt Arg	tcc Ser	tat Tyr	1159

365 370 360 get cet gag ega gee cae ege ega gag ace ate gag etg tgg aac aag 1207 Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys 375 380 385 att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val 390 395 400 gat cot goa gaa aag goo tto ggo goa cgo goa gtg ato aco tto aag 1303 Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys 420 410 415 1351 gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro 425 430 ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc 1399 Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg 445 440 acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg 1447 Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu 455 gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac 1495 Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn 480 470 475 att qaa ttq qat qcc qat att ttq qcc aag qct cct qtq att ccq gaa 1543 Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu 490 495 1575 gga ctg ttc tgatggcggg tttgttttcc tct Gly Leu Phe <210> 602

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Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser 50 55 60

Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly 65 70 75 80

Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala

85 90 95

Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe 100 105 110

Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu 115 120 125

Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly 130 135 140

Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys 145 155 160

Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro Ser Ala 165 170 175

Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr 180 185 190

Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser 195 200 205

Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala 210 215 220

Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly 225 230 235 240

Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu 245 250 255

Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly 260 265 270

Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala 275 280 285

Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu 290 295 300

Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val 305 310 315 320

Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly Ser Asn $325 \hspace{1.5cm} 330 \hspace{1.5cm} 335$

Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His 340 345 350

Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His 355 360 365

His Glu Arg Ser Tyr Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile 370 375 380

Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg 385 390 395 400

Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala 405 410 415

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val 420 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr 440 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp 470 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala 490 485 Pro Val Ile Pro Glu Gly Leu Phe 500 <210> 603 <211> 975 <212> DNA <213> Çorynebacterium glutamicum <220> <221> CDS <222> (1)..(975) <223> FRXA00406 <400> 603 gac cca gtt gag gtt gct gcg gac act cag gaa atg atc atc acc cgc 48 Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca 96 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt 144 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg 192 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac 240 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp 288 acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro 90 att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc 336 Ile Leu Ala Ala Gln Gln Ala Gly Lys Gly Lys Asp Leu Ile 105 cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga 384 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly

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Ala 65	Ala	Leu	Ala	Asn	Gly 70	Thr	Ala	Val	Arg	Glu 75	Leu	Asp	Phe	His	Asp 80
Thr	Phe	Leu	Ala	Ala 85	Glu	Tyr	Ser	His	Pro 90	Gly	Asp	Asn	Ile	Pro 95	Pro
Ile	Leu	Ala	Ala 100	Ala	Gln	Gln	Ala	Gly 105	Lys	Gly	Gly	Lys	Asp 110	Leu	Ile
Arg	Gly	Ile 115	Ala	Thr	Gly	Tyr	Glu 120	Ile	Gln	Val	Asn	Leu 125	Val	Arg	Gly
Met	Cys 130	Leu	His	Glu	His	Lys 135	Ile	Asp	His	Val	Ala 140	His	Leu	Gly	Pro
Ser 145	Ala	Ala	Ala	Gly	Ile 150	Gly	Thr	Leu	Leu •	Asp 155	Leu	Asp	Val	Asp	Thr 160
Ile	Tyr	Gln	Ala	Ile 165	Gly.	Gln	Ala	Leu	His 170	Thr	Thr	Thr	Ala	Thr 175	Arg
Gln	Ser	Arg	Lys 180	Gly	Ala	Ile	Ser	Ser 185	Trp	Lys	Ala	Phe	Ala 190	Pro	Ala
Phe	Ala	Gly 195	Lys	Met	Ser	Ile	Glu 200	Ala	Val	Asp	Arg	Ala 205	Met	Arg	Gly
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Glu	Gly	Glu	Ala	Lys 245	Arg	Ala	Ile	Leu	Asp 250	Thr	Tyr	Thr	Lys	Glu 255	His
Ser	Ala	Glu	Tyr 260	Gln	Ser	Gln	Ala	Pro 265	Ile	Asp	Leu	Ala	Arg 270	Ser	Met
Gly	Glu	Lys 275	Leu	Ala	Ala	Gln	Gly 280	Leu	Asp	Leu	Arg	Asp 285	Val	Asp	Ser
Ile	Val 290	Leu	His	Thr	Ser	His 295	His	Thr	His	Tyr	Val 300	Ile	Gly	Thr	Gly
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Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
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cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca
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Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
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Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
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                                                                   288
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
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cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat
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Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
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ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct
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Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
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Val Ile Thr Ph 50	e Lys Asp	Gly Thr Val 55	Val Glu Ası 60		Ala Val	
Ala Asn Ala Hi 65	s Pro Leu 70	Gly Ala Arg	Pro Phe Ala	a Arg Glu	Gln Tyr 80	
Ile Gln Lys Ph	e Arg Thr 85	Leu Ala Glu	Gly Val Vai	l Ser Glu	Lys Glu 95	
Gln Asp Arg Ph		Ala Ala Gln 105	Arg Thr His	s Glu Leu 110	Glu Asp	
Leu Ser Glu Le 115	u Asn Ile	Glu Leu Asp 120	Ala Asp Ile	e Leu Ala 125	Lys Ala	
Pro Val Ile Pr 130	o Glu Gly	Leu Phe 135	١			
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acc act gat gt Thr Thr Asp Va						163
gcc gtt tcc aa Ala Val Ser Ly 2						211
tac gcg gtg ga Tyr Ala Val Gl 40						259
tac ctc ctg to Tyr Leu Leu Tr 55				n Gln Leu		307
ttc aat gag co Phe Asn Glu Ar 70						355

						ccc Pro										403
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						cgc Arg										499
	_	-			-	atg Met 140	-		-	_	-					547
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Gln 65	Gln	Leu	Ala	Glu	Phe 70	Asn	Glu	Arg	Gly	Arg 75	Ser	Tyr	Arg	Ser	Leu 80	
Asp	Ala	Gly	Leu	Ile 85	Ser	Leu	Ile	His	Ser 90	Leu	Pro	Lys	Glu	Ala 95	His	
Pro	Met	Asp	Val 100	Met	Arg	Thr	Ala	Val 105	Ser	Tyr	Met	Gly	Thr 110	Lys	Asp	
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Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe 35 40 45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly 50 55 60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg 65 70 75 80

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- gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc $\,$ 163 Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro $\,$ 10 $\,$ 15 $\,$ 20
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- ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307 Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly 55 60 65
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	aac Asn															931
	cgc Arg															979
	act Thr 295															1027
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Ala 145	Lys	Gly	Phe	Asp	His 150	Thr	Thr	Gln	Gly	Ala 155	Phe	Ala	Ala	Gly	Ala 160
Ser	Ala	Ala	Lys	Ala 165	Leu	Gly	Leu	Pro	Ala 170	Asp	Gln	Ile	Ala	Asn 175	Ala
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Gly	Asn	Leu 195	Ser	His	Trp	Lys	Gly 200	Leu	Ala	Tyr	Pro	His 205	Val	Ser	Lys
Glu	Gly 210	Thr	Trp	Ala	Ala	Leu 215	Leu	Ala	Ser	Arg	Gly 220	Ile	Thr	Gly	Pro
Glu 225	Glu	Val	Phe	Glu	Gly 230	Asn	Lys	Gly	Phe	Lys 235	Glu	Ser	Val	Ser	Gly 240
Pro	Phe	Glu	Ile	Asp 245	Trp	Ser	Lys	Glu	Asp 250	Leu	Glu	Ser	Val	Lys 255	Arg
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Gln	Leu	Asn	Pro 340	Glu	Gln	Tyr	Glu	Pro 345	Ser	Arg	Ile	Val	Ala 350	Asp	Asp
Val	Gln	Thr 355	Leu	Met	Lys	Lys	Ile 360	Glu	Ile	Thr	Pro	Ser 365	Asp	Glu	Phe
Ser	Asp 370	Arg	Phe	Pro	Asp	His 375	Met	Pro	Ala	Asp	Leu 380	Glu	Val	Thr	Leu
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His	Asp	Asn	Pro	Leu 405	Asp	Trp	Asp	Asn	Ala 410	Arg	Lys	Lys	Phe	Asp 415	Ala
Leu	Val	Thr	Pro	Phe	Thr	Gly	Glu	Glu	Leu	Arg	Glu	Glu	Ile	Ala	Thr

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Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
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Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
50 55

cat gtg cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag 240 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu 65 70 75 80

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Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
85 90 95

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				ctt Leu 10												163

					gag Glu		_		_				-		_	211
					atc Ile											259
	-		_	-	ttg Leu	-						_				307
					cgg Arg 75											355
					gag Glu											403
_	_	_	-		cac His	-				-	-	•				451
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170

528

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Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr

165

603

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gcc aat gag Ala Asn Glu 230	_	-		_	_	-		-	-			835
aat gct gcc Asn Ala Ala												883
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tcc atg gag Ser Met Glu 280												979 •
aaa tgg gtg Lys Trp Val 295			Ser									1027
act ggc att Thr Gly Ile 310			-		_	_			-			1075
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cga gtg tca Arg Val Ser												1171
gcg ctg atc Ala Leu Ile 360	-	_	-					-	_			1219
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Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu 50 60

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Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp 85 90 95

Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro 100 105 110

Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu 115 120 125

Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Ser Gly 130 135 140

Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe 145 150 155 160

Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala 165 170 175

Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His 180 185 190

Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg 195 200 205

Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly 210 215 220

Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp 225 230 235 240

Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp 245 250 255

Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly 260 265 270

Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala 275 280 285

Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu 290 295 300

Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala 305 310 315 320

Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro 325 330 335

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Gln Phe Glu Asn Asn Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly 355 360 365

Val Glu Glu Arg Glu Val Val Pro Ile Ser Glu Arg Thr

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135

150

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aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc

Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala

gtc tcg gcc cgg cgc gac ccg aac ttt gtc atc tgc gcc cgc acc gac Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp

155

130

547

gcc gct gga Ala Ala Gly												643
tac tta gat Tyr Leu Asp												691
gaa gcc gac Glu Ala Asp 200												739 [.]
ctg gcg aat Leu Ala Asn 215		Glu P										787
gtg ttg gaa Val Leu Glu 230												835
ctg cgt att Leu Arg Ile												883
gaa cac ggt Glu His Gly		_		-	_	_	_			_	_	931
aga tta tat Arg Leu Tyr 280		_	-	-	-			-		_	_	979
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Phe Lys Ala	33 - 7	77 - 7	la Pro	112 -	Ile	Ala	Ara	Leu	Pro	Gly	Ala	
	20	Ala A	ia Fio	25			9		30			
Phe Ser Pro 35	20			25						Glu	Gly	
	20 Leu Ile	Ala A	rg Ser 40	25 Ile	Glu	Glu	Ala	Gly 45	Phe			

Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala 105 Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys 120 Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg 135 Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile 170 165 Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr 185 Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile 195 200 Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr 215 Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr 280 Asn Val Phe Asp Gln His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn Glu 305 <210> 623 <211> 242 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(219) <223> FRXA02333 <400> 623 gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg ctg cgt att Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile

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	caa Gln															144
	ctc Leu 50															192
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gac																242
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Thr	Gln	Glu 35	Gly	Trp	Leu	Asp	Arg 40	Met	Gln	His	Arg	Ser 45	Arg	Leu	Tyr	
Glu	Leu 50	Leu	Arg	Tyr	Glu	Asp 55	Tyr	Asn	Val	Phe	Asp 60	Gln	His	Ile	Phe	
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ctci	tctgo	cac a	aatgt	ttct	t to	ggaa	ctat	: tct	ggcg	jacc				gaa Glu		115
	agc Ser				Asp											163

	aag Lys															211
cgc Arg	tgg Trp	ttg Leu 40	act Thr	gtt Val	gtt Val	gat Asp	cca Pro 45	gaa Glu	aac Asn	cca Pro	gat Asp	ggt Gly 50	gtg Val	cag Gln	ctt Leu	259
ttg Leu	ttg Leu 55	gaa Glu	cca Pro	aac Asn	cag Gln	cac His 60	cca Pro	gat Asp	gca Ala	gcg Ala	act Thr 65	tac Tyr	caa Gln	gct Ala	gga Gly	307
	aaa Lys															355
cag Gln	gaa Glu	gaa Glu	tat Tyr	gac Asp 90	agc Ser	ctc Leu	aag Lys	gat Asp	aaa Lys 95	ggc Gly	gtg Val	gat Asp	ttc Phe	atc Ile 100	atg Met	403
gaa Glu	cca Pro	acc Thr	gat Asp 105	gtg Val	ggc Gly	cct Pro	tca Ser	gtg Val 110	att Ile	gcc Ala	att Ile	ctc Leu	gat Asp 115	gac Asp	acc Thr	451
-	gga Gly				-		-		_	-	_		taad	cccc	gtg	500
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Leu	Asp	Phe	Tyr 20	Thr	Thr	Lys	Leu	Gly 25	Phe	Glu	Leu	ГЛЗ	His 30	Asp	Val	
Thr	Ala	Gly 35	Asp	Tyr	Arg	Trp	Leu 40	Thr	Val	Val	Asp	Pro 45	Glu	Asn	Pro	
Asp	Gly 50	Val	Gln	Leu	Leu	Leu 55	Glu	Pro	Asn	Gln	His 60	Pro	Asp	Ala	Ala	
Thr 65	Tyr	Gln	Ala	Gly	Ile 70	Lys	Arg	Asp	Gly	Ile 75	Pro	Ala	Thr	Gln	Phe 80	
							-	(T)	7.00	807	Ton	Luc	Aen	T	C1	
Tyr	Val	Asp	Asp	Val 85	Gln	Glu	GIU	Tyr	90	261	Leu	цуз	изр	95	GTÀ	
	Val Asp			85					90					95		

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165

Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly

150

				att Ile 170												643
				gag Glu												691
				gtg Val												739
atg Met	cgc Arg 215	atc Ile	att Ile	tcc Ser	aac Asn	atc Ile 220	ttt Phe	gag Glu	tac Tyr	acc Thr	tcc Ser 225	ttg Leu	aag Lys	atg Met	cca Pro	787
				att Ile												835
		-	-	ttg Leu 250		-	-			-						883
				ggt Gly												931
				ttc Phe												979 ·
	-	-	_	cgt Arg			_	_	_		_		_		-	1027
				aaa Lys												1075
		Ser	Gly	tgg Trp 330	Ser	Leu		Ala	Gln	Asp	Val	Tyr	Asn			1123
gcc Ala	cgc Arg	acc Thr	gcg Ala 345	att Ile	gag Glu	gcg Ala	atg Met	gct Ala 350	gca Ala	acc Thr	cag Gln	ggc Gly	cac His 355	acc Thr	cag Gln	1171
tcg Ser	ctg Leu	cac His 360	acc Thr	aat Asn	gca Ala	ctt Leu	gat Asp 365	gag Glu	gcg Ala	ttg Leu	gcg Ala	ctg Leu 370	ccc Pro	acc Thr	gat Asp	1219
				atc Ile												1267
				cgt Arg												1315

gag t Glu T	gg (ttg Leu	acc Thr	aat Asn 410	gag Glu	ctg Leu	gct Ala	aac Asn	cgc Arg 415	gcg Ala	cgc Arg	aag Lys	cac His	atc Ile 420	gat Asp	1363
gag g Glu V																1411
cct a Pro L	ys :	ctg Leu 440	cgc Arg	att Ile	gag Glu	gaa Glu	tca Ser 445	gcg Ala	gca Ala	cgc Arg	acc Thr	cag Gln 450	gct Ala	cgc Arg	att Ile	1459
gat t Asp S 4																1507
gaa g Glu A 470																1555
gca g Ala G																1603
gcg g Ala G																1651
gag c Glu H	lis	aaa Lys 520	gag Glu	cca Pro	Gly	gat Asp	ttg Leu 525	gat Asp	cag Gln	aac Asn	ctg Leu	ctc Leu 530	aaa Lys	ctt Leu	gcc Ala	1699
gtc g Val A 5																1747
ttg g Leu G 550																1795
ggc g Gly V	gtg /al	tac Tyr	Lys	gat Asp 570	gag Glu	gtt Val	gga Gly	Lys	gaa Glu 575	Gly	aca Thr	gtg Val	agc Ser	aac Asn 580	gtc Val	1843
gaa c Glu A																1891
cgc c Arg P	ro .															1939
gga c Gly G 6																1987
gat g Asp V 630			_	_					_	-	-	-				2035
gtg g	jac	gcc	gat	gtt	cac	gtg	gtg	ggt	atg	tct	tcg	ctg	gca	gca	ggc	2083

	la Asp	Val 650	His	Val	Val	Gly	Met 655	Ser	Ser	Leu	Ala	Ala 660	Gly	
cac ctc a His Leu T	cc ttg hr Leu 665	ctg Leu	ccc Pro	gag Glu	ctg Leu	aag Lys 670	aaa Lys	gaa Glu	ctt Leu	gca Ala	gct Ala 675	ctt Leu	ggc Gly	2131
cgc gat g Arg Asp A 6														2179
ttc cag g Phe Gln A 695														2227
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Met Thr S	er Ile	5					10	-				. 15		•
Met Thr S 1 Arg Ala S Pro Glu G	er Ile er Glu 20	5 Ser	His	Asn	Val	Asp 25	10	Gly	Lys	Val	Trp 30	15 Asn	Thr	
Met Thr S 1 Arg Ala S Pro Glu G	er Ile er Glu 20 ly Ile 35	5 Ser Asp	His Val Gly	Asn Lys His	Val Arg 40 Pro	Asp 25 Val	Ala Phe	Gly Thr	Lys Gln Leu	Val Ala 45 Pro	Trp 30 Asp	15 Asn Arg	Thr Asp	
Met Thr S 1 Arg Ala S Pro Glu G Glu Ala G	er Ile er Glu 20 ly Ile 35	5 Ser Asp Ala	His Val Gly	Asn Lys His 55	Val Arg 40 Pro	Asp 25 Val	10 Ala Phe Asp	Gly Thr Ser	Lys Gln Leu 60	Val Ala 45 Pro	Trp 30 Asp Gly	Asn Arg	Thr Asp Lys	
Met Thr S 1 Arg Ala S Pro Glu G Glu Ala G 50 Pro Phe M	er Ile er Glu 20 ly Ile 35 ln Ala et Arg	5 Ser Asp Ala Gly	His Val Gly Pro 70	Asn Lys His 55 Tyr	Val Arg 40 Pro	Asp 25 Val Val	10 Ala Phe Asp Met	Gly Thr Ser Tyr 75	Lys Gln Leu 60 Thr	Val Ala 45 Pro Asn	Trp 30 Asp Gly	15 Asn Arg Gln	Thr Asp Lys Trp 80	
Met Thr S 1 Arg Ala S Pro Glu G Glu Ala G 50 Pro Phe M 65	er Ile er Glu 20 ly Ile 35 ln Ala et Arg	5 Ser Asp Ala Gly Tyr 85	His Val Gly Pro 70 Ala	Asn Lys His 55 Tyr	Val Arg 40 Pro Pro	Asp 25 Val Thr	10 Ala Phe Asp Met Thr 90	Gly Thr Ser Tyr 75	Lys Gln Leu 60 Thr	Val Ala 45 Pro Asn Glu	Trp 30 Asp Gly Gln Ser	Asn Arg Gln Pro Asn 95	Thr Asp Lys Trp 80 Ala	
Met Thr S 1 Arg Ala S Pro Glu G Glu Ala G 50 Pro Phe M 65 Thr Ile A Phe Tyr A Phe Asp L	er Ile er Glu 20 ly Ile 35 ln Ala et Arg rg Gln rg Arg 100	5 Ser Asp Ala Gly Tyr 85 Asn	His Val Gly Pro 70 Ala	Asn Lys His 55 Tyr Gly	Val Arg 40 Pro Pro Phe Ala	Asp 25 Val Val Thr Ser Gly 105	10 Ala Phe Asp Met Thr 90 Gln	Gly Thr Ser Tyr 75 Ala	Lys Gln Leu 60 Thr Ala	Val Ala 45 Pro Asn Glu Leu	Trp 30 Asp Gly Gln Ser Ser	Asn Arg Gln Pro Asn 95	Thr Asp Lys Trp 80 Ala	
Met Thr S 1 Arg Ala S Pro Glu G Glu Ala G 50 Pro Phe M 65 Thr Ile A Phe Tyr A Phe Asp L	er Ile er Glu 20 ly Ile 35 ln Ala et Arg rg Gln rg Arg 100 eu Ala	5 Ser Asp Ala Gly Tyr 85 Asn	His Val Gly Pro 70 Ala Leu His	Asn Lys His 55 Tyr Gly Ala	Val Arg 40 Pro Pro Phe Ala Gly 120	Asp 25 Val Val Thr Ser Gly 105	10 Ala Phe Asp Met Thr 90 Gln Asp	Gly Thr Ser Tyr 75 Ala Lys Ser	Lys Gln Leu 60 Thr Ala Gly Asp	Val Ala 45 Pro Asn Glu Leu Asn 125	Trp 30 Asp Gly Gln Ser Ser 110 Glu	Asn Arg Gln Pro Asn 95 Val	Thr Asp Lys Trp 80 Ala Ala	

Met	Thr	Met	Asn	Gly 165	Ala	Val	Leu	Pro	Ile 170	Leu	Ala	Phe	Tyr	Ile 175	Val
Ala	Ala	Glu	Glu 180	Gln	Gly	Val	Gly	Pro 185	Glu	Gln	Leu	Ala	Gly 190	Thr	Ile
Gln	Asn	Asp 195	Ile	Leu	Lys	Glu	Phe 200	Met	Val	Arg	Asn	Thr 205	Tyr	Ile	Tyr
Pro	Pro 210	Lys	Pro	Ser	Met	Arg 215	Ile	Ile	Ser	Asn	11e 220	Phe	Glu	Tyr	Thr
Ser 225	Leu	Lys	Met	Pro	Arg 230	Phe	Asn	Ser	Ile	Ser 235	Ile	Ser	Gly	Tyr	His 240
Ile	Gln	Glu	Ala	Gly 245	Ala	Thr	Ala	Asp	Leu 250	Glu	Leu	Ala	Tyr	Thr 255	Leu
Ala	Asp	Gly	Ile 260	Glu	Tyr	Ile	Arg	Ala 265	Gly	Lys	Glu	Val	Gly 270	Leu	Asp
Val	Asp	Lys 275	Phe	Ala	Pro	Arg	Leu 280	Ser	Phe	Phe	Trp	Gly 285	Ile	Ser	Met
-	290		Met			295	-				300				
Ser 305	Glu	Leu	Val	Ala	Lys 310	Phe	Asp	Pro	Lys	Asn 315	Ala	Lys	Ser	Gln	Ser 320
Leu	Arg	Thr	His	Ser 325	Gln	Thr	Ser	Gly	Trp 330	Ser	Leu	Thr	Ala	Gln 335	Asp
Val	Tyr	Asn	Asn 340	Val	Ala	Arg	Thr	Ala 345	Ile	Glu	Ala	Met	Ala 350	Ala	Thr
Gln	Gly	His 355	Thr	Gln	Ser	Leu	His 360	Thr	Asn	Ala	Leu	Asp 365	Glu	Ala	Leu
	370		Thr	_		375		_			380				
Leu 385	Leu	Gln	Gln	Glu	Ser 390	Gly	Thr	Val	Arg	Pro 395	Val	Asp	Pro	Trp	Ala 400
Gly	Ser	Tyr	Tyr	Val 405	Glu	Trp	Leu	Thr	Asn 410	Glu	Leu	Ala	Asn	Arg 415	Ala
Arg	Lys	His	11e 420	Asp	Glu	Val	Glu	Glu 425	Ala	Gly	Gly	Met	Ala 430	Gln	Ala
Thr	Ala	Gln 435	Gly	Ile	Pro	Lys	Leu 440	Arg	Ile	Glu	Glu	Ser 445	Ala	Ala	Arg
Thr	Gln 450	Ala	Arg	Ile	Asp	Ser 455	Gly	Arg	Gln	Ala	Leu 460	Ile	Gly	Val	Asn
Arg 465	Tyr	Val	Ala	Glu	Glu 470	Asp	Glu	Glu	Ile	Glu 475	Val	Leu	Lys	Val	Asp 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys 485 490 495

Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr 500 505 510

Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn 515 520 525

Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly 530 540

Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu 545 550 555 560

Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly 565 570 575

Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu 580 585 590

Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln $595 \hspace{1.5cm} 600 \hspace{1.5cm} 605$

Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp 610 615 620

Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu 625 630 635 640

Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser 645 650 655

Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu 660 665 670

Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val 675 680 685

Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala 690 695 700

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Glu

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<211> 2098

<212> DNA

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Met	Arg 215	Ile	Ile	Ser	Asn	Ile 220	Phe	Glu	Tyr	Thr	Ser 225	Leu	Lys	Met	Pro	
-					tcg Ser 235							-	-			835
					gag Glu											883
					aaa Lys											931
					ttc Phe											979
atc Ile	gca Ala 295	aag Lys	ctg Leu	cgt Arg	gcg Ala	gga Gly 300	cga Arg	ctg Leu	ctg Leu	tgg Trp	agc Ser 305	gag Glu	ttg Leu	gtg Val	gca Ala	1027
		-	-		aac Asn 315	-	-		-	-	-	-	_		tcg Ser 325	1075 .
					tcg Ser											1123
_	-				gag Glu		_	-	_		-				-	1171
_	-				gċa Ala		-	-		_		-			_	1219
		-			gcc Ala	-			_	-	-	_	_		-	1267
					cca Pro 395											1315
					gag Glu											1363
					ggc Gly											1411
					gag Glu											1459
_			_	_	gcg Ala	_					_		_		_	1507

PCT/IB00/00943 WO 01/00844

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					aaa Lys								1603
					gcg Ala								1651
					ggg Gly								1699
					gca Ala								1747
-	-	-	-		ggc Gly 555	-	-	-	-		 _	_	1795
					gag Glu								1843
					ctg Leu								1891
					att Ile								1939
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<213> Corynebacterium glutamicum

665

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325 330 335 Val Tyr Asn Asn Val Ala Arq Thr Ala Ile Glu Ala Met Ala Ala Thr 345 Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu 360 Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala 390 395 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala 410 Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala 420 Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly 535 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu 545 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp 610 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu

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635

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						cag Gln							691
						gca Ala							739
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						ggc Gly							883
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PCT/IB00/00943 WO 01/00844

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	ag tct ccg lu Ser Pro							7
	ga tgg gca rg Trp Ala				Arg Asn			5
	tg gaa aag eu Glu Lys 490							3
	cg ttg tcc ro Leu Ser 505							1
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	ct gac gct hr Asp Ala							7
	gt gga acg ys Gly Thr				Thr Gly			5
	ag ctc cgc ys Leu Arg 570	Glu Ala	Gly Val		Ile Leu		Gly	3
	ag agc ttt ys Ser Phe 585							1
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Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn 305 310 315 320

Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Ala 325 330 335

Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val 340 345 350

Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn 355 360 365

Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala 370 375 380

Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys 385 390 395 400

Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala 405 410 415

Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu 420 425 430

Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile 435 440 445

Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg 450 455 460

Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu 465 470 475 480

Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln 485 490 495

Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr 500 505 510

Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn 515 520 525

Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln 530 540

Ala Ala Gly Ile Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu 545 550 555 560

Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg 565 570 575

Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala 580 585 590

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Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp

185 190 195

gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc 739
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Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro 50 55 60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln 65 70 75 80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu 85 90 95

Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys 100 105 110

Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp 115 120 125

Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser 130 135 140

Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu 145 150 155 160

Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly 165 170 175

Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly 180 185 190

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Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
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                                     15
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Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
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                         60
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Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Pro Leu Ile Tyr
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115

110

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105

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Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro 130 135 Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro 155 Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala 170 165 Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser 200 195 Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile Glu Pro Ala Gly Val Ala Lys <210> 639 <211> 531 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(508) <223> RXN02461 <400> 639 agaaaatctc aaggcaaaaa acaagccacc ccaatctgtg cgacaatcaa accacagact 60 acgactatta tgtcacgaag aaaccaaaga aagggaaata atg cgc gga cta att Met Arg Gly Leu Ile gtt gac tac gct gqa gta cta gac gga acc gat gag gac cag cgt cgc Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg 211 tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val 25 30 atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu 40 307 ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu 55 60 355 ggc gtc gaa aag cca gag gaa gct ttc cag gcc gcc gca gac gcc Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala 70 75 80 403 ate gae etg eec atg egt gae tge gtg ett gte gae gae teg ate ete

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Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp 65 70 75 80	
Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala 85 90 95	
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Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser 115 120 125	
Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile 130 135 140	
Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro 145 150 155 160	
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Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu 180 185 190	
Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg 195 200 205	
Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His	

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Phe	Val	Gln	Gln 260	Pro	Met	Lys	Met	Ala 265	Ser	Ala	Glu	Ser	Leu 270	Cys	Glu
Thr	Ala	Thr 275	Asp	Pro	Asn	Phe	Ser 280	Ile	Leu	Thr	Ile	Gly 285	Thr	His	Asn
Asn	Cys 290	Asp	Thr	Val	Thr	His 295	Leu	Ile	Asp	Val	Pro 300	Phe	Val	Leu	Pro
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Gln	Leu	Gln	Ala	Ala 325	Ala	Glu	Gln	Ala	Tyr 330	Gly	Pro	Gly	Asn	Tyr 335	Ser
Pro	Asn	Leu	Phe 340	Val	Thr	Tyr	Trp	Ser 345	Phe	Arg	Ala	Met	11e 350	Gly	Leu
Met	Leu	Gly 355	Ser	Leu	Ala	Ile	Ala 360	Ala	Ile	Ala	Trp	Leu 365	Leu	Leu	Arg
Lys	Lys 370	Arg	Thr	Pro	Thr	Gly 375	Lys	Ile	Ala	Arg	Leu 380	Phe	Gln	Ile	Gly
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Ile	Phe	Thr	Glu	Met 405	Gly	Arg	Gln	Pro	Trp 410	Val	Val	His	Pro	Asn 415	Pro
Glu	Ser	Ala	Gly 420	Asp	Ala	Arg	Thr	Glu 425	Met	Ile	Arg	Met	Thr 430	Val	Asp
Met	Gly	Val 435	Ser	Asp	His	Ala	Pro 440	Trp	Gln	Val	Trp	Leu 445	Thr	Leu	Ile
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Val	Glu	Ala	Lys	Thr 485	Gly	Pro	Ala	Thr	Pro 490	Ile	Gly	Ser	Asp	Met 495	Pro

Glu

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Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
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	att Ile 50			-	-			_				-				192
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	gag Glu															288
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	aca Thr	-				_										384
_	gcg Ala 130		_	_	-	_	_	_		_	-			_	-	432
	tcg Ser	_					_		-						-	480
	tct Ser															528
_	ttc Phe			_		_	_	_		_		_		_	_	576
	acc Thr															624
	aac Asn 210															672
	ttc Phe	-	-	-						-		_	-		-	720
	cag Gln						_									768
	cct Pro		_		_						_		_			816

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Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala

40

35

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Pro 225	Phe	Leu	Ala	Glu	Gly 230	Lys	Phe	Thr	Gly	Val 235	Thr	Leu	Gln	Gly	Val 240
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Ser	Pro	Asn	Leu 260	Phe	Val	Thr	Tyr	Trp 265	Ser	Phe	Arg	Ala	Met 270	Ile	Gly
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Pro	Glu	Ser	Ala 340	Gly	Asp	Ala	Arg	Thr 345	Glu	Met	Ile	Arg	Met 350	Thr	Val
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Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly 50 $\,$ 55 $\,$ 60

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Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg 85 90 95

Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln 100 105 110

Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu 115 120 125

Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys 130 135 140

Ala Asp His Thr Ile Asp Ala Ala Ala Leu Pro Gly Met Val Asn 145 150 155 160

Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu 165 170 175

His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr 180 185 190

Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr 195 200 205

Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp 210 215 220

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	aac cag atc tcc acc Asn Gln Ile Ser Thr 445		
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					tcc Ser											1651
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1	1111	Int	IIIL	5 5	His	гуѕ	GIII	Leu	10	116	met	ıyı	116	15	мес	
Ser	Phe	Ser		Phe	Phe	Leu	Gly		Leu	Met	Ala	Leu	Leu	Ile	Arg	
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Asn Thr 65 Gly Ile Gly Ala	Gln 50 Pro Ala Thr Gly Ile 130	35 Leu Ile Pro Thr Ala 115 His	Phe Phe Val Asp Val 100 Ala Ser	Thr Trp Val 85 Gly Asp	Met Gly 70 Ala Gly Phe	His 55 Phe Phe Val Gly Leu 135	40 Gly Ala Pro Ala Trp 120 Gly	Gln Thr Asn Arg Met 105 Thr	Val Tyr Leu 90 Leu Met	Met Val 75 Asn Thr Tyr	Leu 60 Leu Ala Gly Ser Trp 140	45 Leu Pro Phe Phe Ile	Glu Leu Gly Leu 110 Leu Val	Tyr Gln Phe 95 Thr Ser	Gly Ile 80 Trp Pro Asp	

Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile 180 185 Phe Pro Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys 195 200 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala 235 230 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg 250 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly 280 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro 345 Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val 440 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val 450 455 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp 470 475 Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg 490 His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe

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Ala	Glu	Leu 35	Phe	Thr	Pro	Gly	Leu 40	Gln	Phe	Leu	Şer	Asn 45	Glu	Gln	Phe	
Asn	Gln 50	Leu	Phe	Thr	Met	His 55	Gly	Thr	Val	Met	Leu 60	Leu	Leu	Tyr	Gly	
Thr 65	Pro	Ile	Val	Trp	Gly 70	Phe	Ala	Asn	Tyr	Val 75	Leu	Pro	Leu	Pro	Thr 80	
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ctg Leu ttg	tcc Ser	atg Met	gct Ala ttc	gtg Val 10	tgg	gct Ala	cac His	cac His	atg Met 15	ttc Phe ctg	Leu 1 gtt Val att	Ser act Thr	Ile ggc Gly gtt	gca Ala 20 cct	Ala 5 gtt Val	
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ctg Leu ttg Leu ggc Gly act Thr	tcc Ser ctt Leu gtt Val tgg Trp 55	atg Met Ccg Pro aag Lys 40 gaa Glu	gct Ala ttc Phe 25 ttc Phe acc Thr	gtg Val 10 ttc Phe ttc Phe	tgg Trp tcc Ser aac Asn	gct Ala ttc Phe tgg Trp atc Ile 60	cac His atg Met Val 45 tgg Trp	cac His acg Thr 30 gga Gly tct Ser	atg Met 15 ttc Phe acc Thr gtt Val	ttc Phe ctg Leu atg Met ggc Gly	tcc	act Thr tcg Ser aag Lys 50 atg Met	ggc Gly gtt Val 35 ggt Gly gct Ala	gca Ala 20 cct Pro cac His acc Thr	Ala 5 5 gtt Val acc Thr atc Ile ttc Phe gac	163 211 259
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PCT/IB00/00943 WO 01/00844

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45

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				acc Thr												787
				gag Glu												835
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gca atg atg Ala Met Met 295		Glu L										1027
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	g gca t Ala															211
	t gtc r Val															259
	g cta y Leu 55															307
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Met Ser Asn Asn Asn

1

													aat Asn			163
													gca Ala 35			211
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													ctg Leu			403
													gtc Val 115			451
													cgc Arg			499
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													atc Ile			595
			Gly		Ala	Val	Leu	Ala	Gly	Leu	Thr	Ile	atc Ile	Ala		643
													ggc Gly 195			691
													act Thr			739
gag Glu	aac Asn 215	gac Asp	gtc Val	aag Lys	gtt Val	tac Tyr 220	ctc Leu	ggc Gly	cgc Arg	gac Asp	act Thr 225	gca Ala	gca Ala	att Ile	gcg Ala	787
													act Thr			835

						cgc Arg								883
						cca Pro								931
						gtc Val								979
						atg Met 300								1027
						gaa Glu								1075
						att Ile								1123
						aat Asn								1171
		_	_	-		tac Tyr		-		-		-	-	1219
						cca Pro 380								1267
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<213> Corynebacterium glutamicum

<400> 666

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Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val 20 25 30

Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala 35 40 45

Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile

50 55 60

Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr 90 Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser 200 Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp 215 Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp 230 235 Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu , Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val 265 Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile 330 Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys 340 Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val 360

Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp

375

370

Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly

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ctc gtc ggc tgg gc Leu Val Gly Trp Al 150	a gtg atc gt a Val Ile Va 155	t gat cag ttt gag l Asp Gln Phe Glu 160	cca ggc gtt cca 595 Pro Gly Val Pro 165
cag cag tgg tgg ca Gln Gln Trp Trp Gl 17	n Ala Ile Va	c ctg ttc atg gtg l Leu Phe Met Val 175	att ttc ttc tgg 643 . Ile Phe Phe Trp 180
acc cca cct cac ac Thr Pro Pro His Th 185			
aag gcg gct ggc gt Lys Ala Ala Gly Va 200		ı Pro Val Val Arç	
gtc acc gca caa at Val Thr Ala Gln Il 215			Val Leu Thr Thr
ttc ttg ctc atc co Phe Leu Leu Ile Pr 230			
att tcc ggc gtc ac Ile Ser Gly Val Th 25	r Phe Leu Ph		
atc aaa aac ggt gg Ile Lys Asn Gly Gl 265			
aac aac tac ttg go Asn Asn Tyr Leu Al 280		e Val Ala Leu Ser	
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Glu Leu Leu Leu Va 20	l Ala Thr Ile	e Pro Thr Met Leu 25	Gln Ala Glu Arg 30
Gly Glu Asn Asn Il	e Val Leu Ile 40		Phe Gly Gly Trp
Met Gly Ala Ala Al	a Ala Asn Th	r Phe Asn Met Val	Ala Asp Ser Asp

50 55 60

Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His
65 70 75 80

Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val 85 90 95

Ala Ser Phe Leu Trp Leu Trp Leu Cys Asp Ser Met Leu Ala Gly
100 105 110

Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys 115 120 125

Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala

Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe 145 150 155 160

Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met 165 170 175

Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys 180 185 190

Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val 195 200 205

Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala 210 215 220

Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr 225 230 235 240

Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile 245 250 255

Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys 260 265 270

Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu 275 280 285

Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly 290 295 300

Trp Thr Thr Thr Phe Phe 305 310

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215 220 225 ate cac ggc tac agc atg tac atc tac ctc ttc atc ctc atc gtg 835 Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val 230 235 240 Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu 250 255 260 ggc ctc atg ctg att ctg ttc att ctg att cag gca ggt atc ggc atc 931 Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile 265 270 ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile 285 280 gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag 1027 Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln 295 300 ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat 1075 Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp 315 310 ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser aag cag cct gtt aaa taacacgcaa ctgtatcggt aaa 1161 Lys Gln Pro Val Lys 345 <210> 670 <211> 346 <212> PRT <213> Corynebacterium glutamicum <400> 670 Val Ser Thr Ser Asp Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala 90 Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Glu 100 105

Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala
115 120 125

Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val 130 135 140

Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile 145 150 155 160

Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr 165 170 175

Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu 180 185 190

Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His 195 200 205

Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile 210 215 220

Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe 225 230 235 240

Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys 245 250 255

His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln 260 265 270

Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser 275 280 285

Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser 290 295 300

Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val 305 310 315 320

Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro 325 330 335

Phe Glu Lys Lys Ser Lys Gln Pro Val Lys 340 345

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Met Thr Tyr Thr Ile gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt 163 Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys 211 ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa 259 Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu 45 307 gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr 60 355 ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala 80 gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg 403 Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu 90 ccg cca cag aac cag aac taggacctga tatcggccct aaa 444 Pro Pro Gln Asn Gln Asn 105 <210> 672 <211> 107 <212> PRT <213> Corynebacterium glutamicum

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20 25 30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro 35 40 45

Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu 50 60

Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly 65 70 75 80

Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln 85 90 95

Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn 100 105

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ttattagcct cttagagttc tcaggagaaa acgaaatccc atg aca tac aca atc
                                                                   115
                                             Met Thr Tyr Thr Ile
gca cag ccc tgc gtt gac gtc ttg gat cgt gcc tgc gtt gaa gaa tgc
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
                 10
cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg
                                                                   211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
             25
                                  30
qat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag
                                                                   259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu
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                             45
gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac
                                                                   307
Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn
     55
                         60
                                                                   355
gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg
Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
70
                     75
gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg
                                                                   403
Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu
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                                                         100
ccg cct cag gca taatctaacg catgacctct cgc
                                                                   438
Pro Pro Gln Ala
            105
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Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
         35
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Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu

55

50

60

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355 gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile

Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn

55

gaa Glu														403
gga Gly														451
cct Pro														499
ctg Leu														547
gtc Val 150	-	-	•	_	_						_	-	-	595
gcg Ala														643
ggt Gly														691
ttc Phe											ctt Leu			739
Arg											ggc Gly			787
cta Leu 230											gtg Val			835
ggt Gly		Pro	Asn		Ğlu	Leu	Åla	Ala	Val				Ile	883
aac Asn														931
acc Thr											atc Ile			979
Ser											aac Asn			1027
gag Glu 310					Āla									1075

													ctc Leu			1123
													atc Ile 355		cag Gln	1171
-		-		-	_			_				_	ggc Gly	-		1219
													atg Met		gtg Val	1267
-	-	•									-	-	ctt Leu	-	-	1315
-		-	_	-	-				_	-	-	_	gag Glu	-		1363
cga Arg	tgad	ctcg	cag t	aati	taco	ec go	et									1389

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<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

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Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro 35 40 45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu 50 60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val 65 70 75 80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly 85 90 95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu 100 105 110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu 115 120 125

Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys 130 135 140

Ala 145	Met	Ile	Gly	Ser	Val 150	Thr	Asp	Ala	Val	Val 155	Val	Gly	Gly	Gly	Phe 160
Ile	Gly	Leu	Glu	Ala 165	Ala	Cys	Ser	Leu	His 170	Asp	Leu	Gly	Lys	Asn 175	Val
Thr	Val	Leu	Glu 180	Tyr	Gly	Pro	Arg	Leu 185	Ile	Gly	Arg	Ala	Val 190	Gly	Glu
Glu	Thr	Ala 195	Ala	Phe	Phe	Leu	Glu 200	Gln	His	Arg	Ser	Arg 205	Gly	Val	Asn
Ile	Val 210	Leu	Asp	Ala	Arg	Met 215	Lys	Gln	Phe	Val	Gly 220	Lys	Asp	Gly	Lys
Leu 225	Ser	Gly	Ile	Glu	Leu 230	Glu	Asp	Gly	Thr	Val 235	Ile	Pro	Ala	Gln	Leu 240
Val	Ile	Val	Gly	Ile 245	Gly	Val	Ile	Pro	Asn 250	Thr	Glu	Leu	Ala	Ala 255	Val
Leu	Gly	Leu	Asp 260	Ile	Asn	Asn	Gly	11e 265	Val	Val	Asp	Lys	His 270	Ala	Val
Ala	Ser	Asp 275	Gly	Thr	Thr	Ile	Ala 280	Ile	Gly	Asp	Val	Ala 285	Asn	Ile	Pro
Asn	Pro 290	Ile	Pro	Gly	Ser	Pro 295	Ala	Asp	Glu	Arg	Ile 300	Arg	Leu	Glu	Ser
Val 305	Asn	Asn	Ala	Ile	Glu 310	His	Ala	Lys	Ile	Ala 315	Ala	Tyr	Ser	Leu	Val 320
Gly	Gln	Pro	Glu	Ala 325	Tyr	Ala	Gly	Ile	Pro 330	Trp	Phe	Trp	Ser	Asn 335	Gln
Gly	Asp	Leu	Lys 340	Leu	Gln	Ile	Ala	Gly 345	Leu	Thr	Leu	Gly	Tyr 350	Asp	Ser
Thr	Val	Ile 355	Arg	Gln	Asp	Pro	Glu 360	Lys	Lys	Lys	Phe	Ser 365	Val	Leu	Tyr
Tyr	Arg 370	Gly	Asp	Asn	Ile	Ile 375	Ala	Ala	Asp	Cys	Val 380	Asn	Ala	Pro	Leu
Asp 385		Met	Ala	Val	Arg 390	Ser	Ala	Leu	Ser	Arg 395	Asn	Gln	Asn	Ile	Pro 400
Ala	Asp	Leu	Ala	Ala 405	Asp	Ile	Ser	Gln	Pro 410	Leu	Lys	Lys	Leu	Ala 415	Val
Asp	Leu	Glu	Val 420	Thr	Arg										

<210> 679

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

PCT/IB00/00943 WO 01/00844

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Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp

ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt

Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac

Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct

Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala

ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc Gly Arg Leu Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val

gga atc aat gcc qac cqc acc qca caq caq tcc att ttc ggc qac acc Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg

Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc

Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca

Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc

190

125

45

60

75

155

170

185

90

105

120

135

150

30

115

163

211

307

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403

547

595

643

691

180

Met Ser Ile Ser Tyr

65

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25

40

55

70

175

Lys v	'al	Val 200	Ile	Ala	Gly	Gly	Arg 205	Gly	Val	Gly	Ser	Glu 210	Glu	Asn	Phe	
cgc ac Arg Sc 2																787
gca a Ala Ti 230																835
gtt g																883
ggc a																931
aag g Lys V																979
gcg g Ala A 2																1027
atc galle G					-	-	-	tag	gagti	tt (gaaca	actt	t ta	at .		1074
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<211><212><213><400>Met S 1 Pro V Val A	· 31 · PR · Co · 68 Ser /al	Thr Val Gly	Ser Leu 20 Val Asn	Tyr 5 Glu Val Trp	Val Leu Gly	Leu Ile Glu Ala 55	Val Thr Pro 40 Ala	Glu Ala 25 Gly Gln	10 Ala Ala Val	Arg Gly Val	Ala Val Ser 60	Leu Asn 45 Ala	Gly 30 Leu Glu	15 Asp Ala Ile	Val Ala Ser	
<211><212><213><400>Met S 1 Pro V Val A Glu L Gly A	· 31 · PR · Co · 68 Ger Val	7 TT rryne 60 Ile Thr Val 35 Gly	Ser Leu 20 Val Asn	Tyr 5 Glu Val Trp Arg	Val Leu Gly Gly Leu 70	Leu Ile Glu Ala 55 Ile	Val Thr Pro 40 Ala	Glu Ala 25 Gly Gln Pro	10 Ala Ala Val Ala	Arg Gly Val Val 75	Ala Val Ser 60 Asp	Leu Asn 45 Ala	Gly 30 Leu Glu Leu	15 Asp Ala Ile His	Val Ala Ser Ile 80	
<211><212><213><400>Met S 1 Pro V Val A Glu L Gly A 65	· 31 · PR · Co · 68 Ger /al	7 TT rryne 60 Ile Thr Val 35 Gly Ser	Ser Leu 20 Val Asn Asn	Tyr 5 Glu Val Trp Arg	Val Leu Gly Gly Leu 70	Leu Ile Glu Ala 55 Ile Gly	Val Thr Pro 40 Ala Leu Pro	Glu Ala 25 Gly Gln Pro	10 Ala Ala Val Ala	Arg Gly Val Val 75	Ala Val Ser 60 Asp	Leu Asn 45 Ala Ala	Gly 30 Leu Glu Leu	Asp Ala Ile His Ala 95	Val Ala Ser Ile 80 Ser	

Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser 135 140 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro 155 150 Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys 165 170 Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro 185 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly 200 205 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu 215 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr 230 225 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala 280 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys 310 <210> 681 <211> 909 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(886) <223> RXA00225 <400> 681 gtaggcgtcg aaaagcaatg ggcgaagccc gcgtagtatg ggcgggcaac gctaaaagcg 60 115 ccaaaaacqc caaaaatcqt qaattqaaaq qtqaqtqtgg atg tcc aca atc gtg Met Ser Thr Ile Val 163 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu 15 qct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu

ate aat gag ttt get etg gag eag gea etg ege ttg egg gag tee aac Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met get get aag aag get gag ate aag aag ett tee ttg get gaa ate gge Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr get gea get gat egt eet gag ege tee eaa ggt gat gte att ggt gea Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala

atc tagccactat cttcacaaag gag 909

tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu

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<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

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Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp
20 25 30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg 35 40 45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser 50 55 60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met 65 70 75 80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser 85 90 95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile 100 105 110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser 115 120 125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala 130 135 140

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro 165 170 175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn 180 185 190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser 195 200 205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala 210 215 220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly 225 230 235 240

Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu 245 250 255

Ala Ser Glu Asn Leu Ile 260

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Ser	Lys	Glu	Gly 190	Met	Ile	Thr	Ala	Phe 195	Met	Asp	Ala	Pro	Ile 200	Gly	Asn	
		-	-	tta Leu	_	-	_		_				-	-		735
				tcc Ser												783
				tca Ser												831
				cct Pro 255												879
_			-	gcc Ala		-		-	-	-			-			927
•				atg Met		_	-	_								975
-	-			ttg Leu			_		_						_	1023
				ctg Leu												1071
				gac Asp 335												1119
-				ttc Phe		_	_	-	_	_	_	-		_		1167
		_	-	ctc Leu			-				_	_	_		-	1215
				tcg Ser												1263
_			-	ctc Leu		_		-						-		1311
	_			acc Thr 415	_		-		_	-	_					1359
	-			ggt Gly	_			-	_			_		-		1407

435 440 430 gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc 1455 Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile 450 445 atc atg atg gtt gtc cgg cac cag cct gcc aac ttc aag cgc atc aag 1503 Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys 460 465 ccc age aga agg ege age acc gtt ett gte gee gte ett get gee tte 1551 Pro Ser Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe 475 480 gee gea tte atg geg gtg tgg gga ttg ett gge egt cae gaa egt tet Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser 495 gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly 510 gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg 1695 Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr 530 535 . 525 1743 ttq qqc qaq ctc tcc qtq ctt ggc atg gca gct gtc gtc atc ggt gcg Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala 540 545 atq qtq qct tcc atq cct cgt cat ccg ttt gcc aag ggc acc cac cct 1791 Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro 560 555 cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg 1839 Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu 575 ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc 1887 Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe 590 atg cgt gga cac aat gat ccg gga ggc ggt ttc atc gca gcc cta att 1935 Met Arg Gly His Asn Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile gee ggt gge geg etg atg etc etg tac etg tec aag gee aaa gat gge 1983 Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly 620 625 2031 ege att tte ege eeg aat gtt eet tte att ete aet ggt geg gge ate Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile 635 640 645 2079 ttg atg gca gtg ttc tcg ggc gta ctg gga ctc acc cac ggt tct ttc Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe 655 660 ctg tac qcc atc cac ttc aac ttc gta ggc cag cac tgg acc acc tcg

Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser

675

670

atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser 685 690 695	2175
atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn 700 705 710	2223
gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro 715 720 725 730	2271
acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc ' Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile 735 740 745	2319
aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg 750 755	2365
actgacagtc gcg	2378
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Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys 35 40 45	
Ala Gly Ile Tyr Leu Leu Arg Phe Ser Ile Val Phe His Asp Val 50 55 60	
Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile 65 70 75 80	
Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr 85 90 95	
Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly 100 105 110	
Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser 115 120 125	
His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp 130 135 140	
His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys 145 150 155 160	
Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met	

175 165 170 Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile 185 Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu 200 Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His 230 235 Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro 265 260 Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His 280 Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arq Ala Asn Leu Leu Gly Lys Phe Phe Gly 345 Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val 375 Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Ile Ile Met Met Val Val Arg 450 His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser

495

Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val

485

Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr 520 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arq Met Leu Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp 600 605 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met 615 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn 635 630 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg 755 <210> 685 <211> 1872 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS

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<223> FRXA00606

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					gat Asp											7 87
					ttc Phe 235											835
					ggt Gly											883
cta Leu	ctt Leu	ctg Leu	ggc Gly 265	gct Ala	ccc Pro	gat Asp	gtt Val	gca Ala 270	ctt Leu	acc Thr	cag Gln	ttc Phe	ctg Leu 275	gta Val	gaa Glu	931
					atc Ile											979
		-	-		aag Lys		-	-		-	_		-		-	1027
-	-		_	-	ttc Phe 315	-	-		_					_		1075
					tct Ser											1123
					ggc Gly											1171
					acg Thr											1219
			Ile	Gly	gcg Ala	Met	Val	Ala	Ser	Met		Arg				1267
					cct Pro 395											1315
					ctg Leu											1363
					ttc Phe											1411
					att Ile											1459
tcc	aag	gcc	aaa	gat	ggc	cgc	att	ttc	cgc	ccg	aat	gtt	cct	ttc	att	1507

Ser Lys 455	Ala Lys	Asp Gly	Arg 460	Ile	Phe	Arg	Pro	Asn 465	Val	Pro	Phe	Ile	
ctc act Leu Thr 470	ggt gcg Gly Ala	ggc ato Gly Ile 475	Leu	atg Met	gca Ala	gtg Val	ttc Phe 480	tcg Ser	ggc Gly	gta Val	ctg Leu	gga Gly 485	1555
ctc acc Leu Thr	cac ggt His Gly	tct ttc Ser Phe 490	ctg Leu	tac Tyr	gcc Ala	atc Ile 495	cac His	ttc Phe	aac Asn	ttc Phe	gta Val 500	ggc Gly	1603
cag cac Gln His													1651
gtg ttg Val Leu													1699
cgc cca Arg Pro 535	ggt acc Gly Thr	gac aat Asp Asr	gca Ala 540	gat Asp	ctg Leu	gac Asp	tac Tyr	gcc Ala 545	cgc Arg	cga Arg	agt Ser	ggc Gly	1747
cca ctg Pro Leu 550			Thr										1795
gac tgg Asp Trp													1843
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<400> 686

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Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu

Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser

Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser

His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro

Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala

Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met

100 105 110 His Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu 120 Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu 135 Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe 165 170 Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu 185 Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser 195 200 Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu 215 Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr 230 Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val 280 Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala 315 Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln 390 Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val

430

Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn

425

420

Asp Pro Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu 435 440 Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro 455 Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe 470 475 Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His 490 Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu 500 505 Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly 520 Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr 535 530 Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg 580 <210> 687 <211> 1653 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1630) <223> RXN00595 <400> 687 cgacgacacc cggtccatcg aaccagatga cgatcaatcg cctttgacta ctagcgctcg 60 ttcagtcacc aacccaacag atcaggagga taaagcttaa atg gcc atg gat gtt Met Ala Met Asp Val ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala 10 15 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val 259 cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala 45

gaa Glu	cac His 55	ggc Gly	ccg Pro	att Ile	gct Ala	cac His 60	aac Asn	gtg Val	ggc Gly	ctt Leu	tat Tyr 65	gtc Val	ggt Gly	ggc Gly	gtg Val	307
		ccc Pro														355
acc Thr	tcg Ser	atc Ile	gtt Val	gcg Ala 90	gtg Val	gct Ala	gcc Ala	aac Asn	tgg Trp 95	ttt Phe	gcc Ala	acc Thr	atc Ile	gtc Val 100	ggt Gly	403
		cgc Arg														451
		aac Asn 120														499
		gaa Glu		_	_	-					-		-	-		547
	-	tgg Trp		-		_			-			_		-		595
		gcc Ala														643
		ggc Gly														691
		ctg Leu 200	-	-	-	_	_				_		_			739
		gcc Ala														787
		aca Thr														835
		gcg Ala														883
		ccc Pro														931
		gtc Val 280														979
gtc	ctt	gcc	tac	caa	atg	gtc	aac	ggc	atg	cca	ttt	att	ctc	atc	atg	1027

Val	Leu 295	Ala	Tyr	Gln	Met	Val 300	Asn	Gly	Met	Pro	Phe 305	Ile	Leu	Ile	Met	
													gct Ala			1075
													gtg Val			1123
													tcc Ser 355			1171
													ttc Phe			1219
													atg Met			1267
													att Ile			1315
													gca Ala			1363
													gca Ala 435			1411
													aaa Lys			1459
													atc Ile			1507
													ctc Leu			1555
													atc Ile			1603
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ttc																1653
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<400> 688

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Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile 20 25 30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu 35 40 45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu 50 55 60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala 65 70 75 80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
85 90 95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr 100 105 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu 115 120 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly 130 135 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile 145 150 155 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val 165 170 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln 180 185 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val 195 200 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp 210 215 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe 225 230 235 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp 245 250 255

Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala 260 265 270

Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu 275 280 285

Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro 290 295 300

Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala

315

320

305					310					315					320	
Leu	Ala	Ala	Gly	Leu 325	Leu	Tyr	Thr	Leu	His 330	His	Met	Ile	Thr	Ile 335	Ala	
Ala	Leu	Val	Leu 340	Thr	Ser	Gly	Ala	11e 345	Glu	Glu	Thr	Tyr	Gly 350	Thr	Gly	
Met	Leu	Ser 355	Lys	Leu	Ser	Gly	Leu 360	Ala	Arg	Arg	Glu	Pro 365	Val	Val	Ala	
Ala	Val 370	Phe	Ala	Ala	Gly	Ala 375	Phe	Ser	Val	Val	Gly 380	Phe	Pro	Pro	Phe	
Ser 385	Gly	Met	Trp	Gly	Lys 390	Ala	Leu	Ile	Leu	Leu 395	Glu	Ile	Ala	Arg	Val 400	
Gly	Asn	Ile	Ala	Ala 405	Trp	Ile	Ala	Ile	Ala 410	Ala	Ile	Ile	Ile	Ala 415	Ser	
Leu	Gly	Ala	Leu 420	Leu	Ser	Met	Ile	Arg 425	Val	Trp	Arg	Glu	Val 430	Phe	Trp	
Gly	Gly	Ala 435	Met	His	Gln	Arg	Gly 440	Val	Ser	Pro	Gln	Leu 445	Arg	Ile	Ser	
Pro	Ala 450	Lys	Ile	Ala	Pro	Ala 455	Leu	Ser	Leu	Ile	Ile 460	Leu	Ser	Val	Gly	
Met 465	Phe	Ile	Phe	Ala	Gly 470	Pro	Leu	Ile	Asp	Ala 475	Thr	Leu	Thr	Ala	Thr 480	
Asp	Gly	Leu	Leu	Asn 485	Thr	Asp	Ala	Tyr	Gln 490	Gln	Ala	Val	Leu	Gly 495	Glu	
Asn	Ala	Ile	Gly 500	Val	Pro	Ser	Pro	Ser 505	Tyr	Gln	Gly	Gly	Asn 510			•
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ttca	agtca	acc (aacc	caaca	ag at	tcag	gagga	a taa	aagci	ttaa			atg Met			115
					gtt Val											163
gtg	ctt	ctg	ccg	tgg	cgt	ctc	atc	cgc	gat	att	ttg	cac	atc	atc	gtg	211

Val	Leu	Leu	Pro 25	Trp	Arg	Leu	Ile	Arg 30	Asp	Ile	Leu	His	Ile 35	Ile	Val	
cct Pro	ttc Phe	gcg Ala 40	ggt Gly	att Ile	ttt Phe	gct Ala	ggc Gly 45	atc Ile	tgg Trp	ttg Leu	ttt Phe	gca Ala 50	cac His	acc Thr	gct Ala	259
						cac His 60										307
						gat Asp										355
						gct Ala										403
_		_		_		tat Tyr					_	_	_		_	451
						ctg Leu										499
		-		_	_	ctg Leu 140					_		-	_		547
						gcc Ala										595
						ctg Leu										643
_				-		atc Ile	_	_	_		_	-	_			691
		_	_	_		gca Ala	-				_		_			739
						cca Pro 220										787
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<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

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Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu 35 40 45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu 50 55 60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala 65 70 75 80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe 85 90 95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr 100 105 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
115 120 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly 130 135 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile 145 150 155 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val 165 170 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln 180 185 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val 195 . 200 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp 210 215 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe 225 230 235 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile 245 250 255

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<211> 2118

<212> DNA

<213> Corynebacterium glutamicum

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Thr Val 225	Glu	Arg	Leu	Arg 230	Pro	Asn	Thr	Ala	Ala 235	Phe	Gly	Ser	Ala	Asp 240	
acc gcc Thr Ala	tac Tyr	gac Asp	gcc Ala 245	att Ile	ctt Leu	gat Asp	gca Ala	ctg Leu 250	cgt Arg	gt [:] g Val	ctc Leu	tcc Ser	cac His 255	cgc Arg	768
ctg act Leu Thr	Ála			_	_			-		_		_			816
atc ttc Ile Phe															864
gaa caa Glu Gln 290	Ser														912
ttc atc Phe Ile 305															960
gat aac Asp Asn	cgt	ttg Leu	tct Ser 325	gcg Ala	ctg Leu	att Ile	ttg Leu	gtg Val 330	ggt Gly	gtg Val	aca Thr	ggt Gly	tat Tyr 335	ggc Gly	1008
att gcc Ile Ala	Val														1056
cag gtg Gln Val	_														1104
cgt aaa Arg Lys 370	Met	_		-	-	-		_	_	_			_		1152
cgc gtg Arg Val 385															1200
gtc acc Val Thr															1248
tac atg Tyr Met	Gln														1296
aac gta Asn Val															1344
tcc gtc Ser Val 450	Leu														1392
aac cgc Asn Arg															1440

465	470	475	480
ggt cgc cgt tgg ttg Gly Arg Arg Trp Leu 485	Ala Ala Val Asp	acc gaa agg gcg cag Thr Glu Arg Ala Gln 495	aac 1488 Asn
cgc tcg ctg atg gtt Arg Ser Leu Met Val 500	gat gtg gca acg cgc Asp Val Ala Thr Arg 505	atc ctc ttc cct gcc Ile Leu Phe Pro Ala 510	atg 1536 Met
atc atg ttg tct gtg Ile Met Leu Ser Val 515	tac ttc ttc ttc gcc Tyr Phe Phe Phe Ala 520	gga cac aac gcg ccg Gly His Asn Ala Pro 525	ggc 1584 Gly
ggc gga ttc gcc ggc Gly Gly Phe Ala Gly 530	ggc ctt gtt gcc tcc Gly Leu Val Ala Ser 535	ttg gcg ttc gcc ttg Leu Ala Phe Ala Leu 540	cgc 1632 Arg
tac ctt gcc ggt gga Tyr Leu Ala Gly Gly 545	cgt gaa gaa ctt gaa Arg Glu Glu Leu Glu 550	gaa gcg ttg cct atc Glu Ala Leu Pro Ile 555	gac 1680 Asp 560
gcc ggc cgt atc ttg Ala Gly Arg Ile Leu 565	Gly Thr Gly Leu Phe	gtt tct gca act gca Val Ser Ala Thr Ala 575	gtg 1728 Val
		ccg ctg acc tcc cat Pro Leu Thr Ser His 590	
		att cac att gca tcc Ile His Ile Ala Ser 605	
ctg ctc ttt gac ctt Leu Leu Phe Asp Leu 610	ggt gtc tac ctg atc Gly Val Tyr Leu Ile 615	gtc atc ggt ttg acc Val Ile Gly Leu Thr 620	atg 1872 Met
		gac cgc gat gag gaa Asp Arg Asp Glu Glu 635	
cgt aag cag cgt gcg Arg Lys Gln Arg Ala 645	Arg Asp Arg Ala Arg	cgc ttg gcg cgc aac Arg Leu Ala Arg Asn 655	cag 1968 Gln
		agg tcg aac gag aaa Arg Ser Asn Glu Lys 670	
		ggg gca gac aca gaa Gly Ala Asp Thr Glu 685	
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Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly
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Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met 20 25 30

Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
35 40 45

Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala 50 55 60

Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile 65 70 75 80

Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His 85 90 95

Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile 100 105 110

Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr 115 120 125

Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu 130 135 140

Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu 145 150 155 160

Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu 165 170 175

Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val 180 185 190

His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu 195 200 205

Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp 210 215 220

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp 225 230 235 240

Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg 245 250 255

Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val 260 265 . 270

Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly 275 280 285

Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly 300 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu 360 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser 375 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile 395 390 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val 410 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val 420 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr 475 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn 485 490 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met 505 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly 520 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg 535 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp 545 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val 570 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala 600

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met 615 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met 635 630 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser 665 660 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser 680 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu Lys Gln 705 <210> 693 <211> 955 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(955) <223> RXA00909 <400> 693 tegatgtgtg ttgctaactg ggggtggcac gcacgttggc gttgttgttt ggtgtggctc 60 cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt Val Leu Ile Leu Phe ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr 10 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly 30 259 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly 45 307 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat Gly Glu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn 60 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val 80 403 tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp

95 90 100 tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc 451 Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe 105 gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg 499 Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met 120 125 tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt 547 Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly 135 140 tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg 595 Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu 160 155 atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu 170 175 180 691 atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr 185 190 tca age tee tgg gea gat gtg eeg tat att tee get get gee ett 739 Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Ala Leu 200 205 210 atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc 787 Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe 215 220 tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu 230 cac tee gea geg atg gtg aag geg ggt att tae ett gtg get ege ete 883 His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu 250 255 tot coa gao oto aac gta gtt ggt tog tgg tac otg ato ato cog 931 Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Pro 270 265 955 ttg ggc atg ttg acc atg ctc atg Leu Gly Met Leu Thr Met Leu Met 280 <210> 694

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

Val Leu Ile Leu Phe Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro 1 5 10 15

Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu

20 25 30

Val Pro Gly Ile Gly Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly 35 40 45

Thr Phe Lys Asp Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro 50 55 60

Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu 65 70 75 80

Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys 85 90 95

Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala 100 105 110

Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp 115 120 125

Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser 130 135 140

Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser 145 150 155 160

Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu 165 170 175

Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser 180 185 190

Glu Ile Pro Ala Tyr Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser 195 200 205

Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile 210 215 220

Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro 225 230 235 240

Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr 245 250 255

Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr 260 265 270

Leu Ile Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met 275 280 285

<210> 695

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXA00700

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<210> 696

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

Met Ile Asn Ala Ile Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser 1 5 10 15

Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val 20 25 30

Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile 35 40 45

Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser 50 55 60

Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
65 70 75 80

Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Gly Phe 85 90 95

Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro 100 105 110

Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu 115 120 125

Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala 130 135 140

Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys 145 150 155 160

Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
165 170 175

Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val 180 185 190

Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu 195 200 205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu

220

215

210

Gly Arg Ala Phe Phe Thr Ser Val Leu Leu Leu Thr Ala Lys Pro 230 235 Val Leu Gly Ala Leu Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val 250 Glu Arg Asp Phe Gly Glu Ala Gly Val Pro Arg Val <210> 697 <211> 1587 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1564) <223> RXN00483 <400> 697 agacccaaga qtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg 60 tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt Val Leu Val Thr Gly gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala 15 ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp 45 307 gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Tyr Tyr cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Glu Glu 80 caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403 Gln Arq Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile 90 95 451 aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile 110 499 gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile

125

					aca Thr											547
					gca Ala 155											595
					ata Ile											643
					gat Asp											691
					aac Asn											739
					cta Leu											787
					tcc Ser 235											835
					agt Ser											883
					tca Ser											931
_			_		att Ile		_			_						979
					ctg Leu		Leu			Glu		Asp				1027
					cga Arg 315											1075
-			-		gag Glu					_	_		_	-	_	1123
-		-	-		gat Asp		-	-		_	_		_			1171
					gtg Val											1219
cga	ttg	cgg	ggt	atc	gct	gac	aga	ctc	atc	ggc	ggt	cca	ggt	ttg	ggc	1267

Arg 1	Leu 375	Arg	Gly	Ile	Ala	Asp 380	Arg	Leu	Ile	Gly	Gly 385	Pro	Gly	Leu	Gly	
gga d Gly 1 390			~		-						-	-		-		1315
tgg (Trp /																1363
gag a Glu N																1411
aag (Lys (gaa Glu	aat Asn 440	ggc Gly	gga Gly	tgt Cys	act Thr	tat Tyr 445	acc Thr	cag Gln	cgc Arg	gca Ala	ata Ile 450	ttt Phe	gag Glu	ccg Pro	1459
aag (Lys (1507
gcg a Ala : 470																1555
aaa d Lys 1			taat	cgca	aga (gtago	gcgto	ct aa	aa							1587

<210> 698

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 698

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr 1 5 10 15

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys 20 25 30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu 35 40 45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val 50 55 60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp 65 70 75 80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala 85 90 95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro 100 105 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu 115 120 125

Lys	Val 130	Ala	Gln	Ile	Leu	Leu 135	Ala	Gly	Gln	Thr	Pro 140	Ala	Leu	Ile	Leu
Arg 145	Ala	Ala	Thr	Ile	Ile 150	Gly	Ser	Gly	Ser	Ala 155	Ser	Phe	Glu	Ile	Ile 160
Arg	His	Leu	Thr	Glu 165	Arg	Leu	Pro	Arg	Met 170	Ile	Ala	Pro	Gln	Trp 175	Ile
Thr	Asn	Gln	Ile 180	Glu	Pro	Leu	Ala	Ile 185	Arg	Asp	Val	Leu	His 190	Tyr	Leu
Ile	Ser	Ala 195	Ala	Asp	Leu ·	Lys	Asp 200	Pro	Val	Asn	Arg	Ser 205	Cys	Asp	Ile
Gly	Cys 210	Gly	Lys	Ser	Tyr	Glu 215	Phe	Ala	Asp	Leu	Leu 220	Arg	Ile	Tyr	Ala
Asp 225	Val	Arg	Gly	Leu	Lys 230	Arg	His	Val	Asn	Ser 235	Val	Pro	Leu	Asn	Leu 240
Pro	Met	Asp	Lys	Leu 245	Ser	Gly	Leu	Trp	Ile 250	Ser	Leu	Val	Thr	Pro 255	Val
Pro	Phe	Gln	Leu 260	Ser	Phe	Pro	Leu	Ala 265	Gln	Ser	Met	Ala	Glu 270	Asp	Ala
Val	Thr	Glu 275	Glu	His	Ser	Ile	Lys 280	Asp	Ile	Ile	Ser	Asp 285	Pro	Pro	Asp
Gly	Phe 290	Ile	Glu	Tyr	Arg	Glu 295	Ala	Val	Glu	Leu	Ala 300	Leu	Ala	Ala	Glu
Phe 305	Asp	Arg	Gly	Val	Pro 310	Thr	Ser	Trp	Asp	Arg 315	Ser	Trp	Thr	Val	Gln 320
Gln	Pro	Trp	Ala	Gly 325	Gln	Pro	Thr	Asp	Pro 330	Glu	Trp	Ala	Gly	Lys 335	Ala
Val	Tyr	Glu	Asp 340	Val	Arg	Thr	Glu	Asp 345	Thr	Asp	Leu	Arg	Ala 350	Ala	Gln
Val	Trp	Pro 355	Ile	Ile	Glu	Gly	Leu 360	Gly	Gly	Val	Asn	Gly 365	Trp	Tyr	Ser
Ala	Pro 370	Leu	Leu	Trp	Arg	Leu 375	Arg	Gly	Ile	Ala	Asp 380	Arg	Leu	Ile	Gly
Gly 385	Pro	Gly	Leu	Gly	Gly 390	Arg	Arg	Asp	Pro	Arg 395	His	Leu	Lys	Leu	Gly 400
Asp	Arg	Ile	Asp	Trp 405	Trp	Arg	Val	Thr	Glu 410	Ile	Asp	Pro	Pro	His 415	Arg
Leu	Val	Leu	Thr 420	Ala	Glu	Met	Lys	Val 425	Asp	Gly	Gly	Ala	Trp 430	Leu	Ile
Leu	Glu	Val 435	Ala	Asp	Lys	Glu	Asn 440	Gly	Gly	Cys	Thr	Tyr 445	Thr	Gln	Arg

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Val Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile 475 Leu Lys Ala Ala Arg Lys Leu Thr 485 <210> 699 <211> 1587 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1564) <223> FRXA00483 <400> 699 agacccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg 60 115 teccaetttg cattateaag etcaaaaece geaeeggega gtg etg gte aee ggt Val Leu Val Thr Gly 163 gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg ttt gae tgg tae gag gae gte gag gea gtg gaa geg gat etg aet gae 259 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp 45 gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Tyr Tyr cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Glu Glu caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile ttq ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547 Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile

PCT/IB00/00943 WO 01/00844 140 145 135 att ggt tee gge tet gea tea tit gaa ata ate egt cat ete aeg gag 595 Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu 160 150 155 cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag 643 Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 175 691 cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 190 185

tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg 739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser
200 205 210

tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu
215 220 225

aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta 835 Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 240 245

tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct 883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser
250 255 260

ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac 931 Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 275

agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat 979 Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 290

cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt 1027 Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val 295 300 305

cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly
310 315 320 325

cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc 1123 Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val 330 335 340

cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att 1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile
345 350 355

gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg 1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp
360 365 370

cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc 1267 Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly 375 380 385

				cat His							1315
				gat Asp							1363
				ggc Gly							1411
				act Thr							1459
				ctc Leu 460							1507
				atg Met							1555
ctc Leu	taa	tege	aga (gtag	gcgto	ct aa	aa				1587

<210> 700 <211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr 1 5 10 15

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys 20 25 30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu 35 40 45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val 50 55 60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp 65 70 75 80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala 85 90 95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro 100 105 . 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu

PCT/IB00/00943

WO 01/00844 140 130 135 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile 155 150 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile 170 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu 235 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val 250 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala 260 / 265 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp 280 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg 410

Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile 420 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg 440 Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val 455 450

1000

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile

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Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp 190 gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg 739 Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu 205 agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act 787 Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta 835 Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu 1003

				235					240					245	
gtg ctc Val Leu															883
aaa gcg Lys Ala															931
aac act Asn Thr	cct Pro 280	gat Asp	atg Met	ggt Gly	gaa Glu	caa Gln 285	ggg Gly	aaa Lys	att Ile	ctg Leu	aat Asn 290	aag Lys	atc I l e	gcc Ala	979
gac atg Asp Met 295	Val	gat Asp	cgg Arg	ggt Gly	cag Gln 300	ttt Phe	gag Glu	tcc Ser	gtg Val	aca Thr 305	gca Ala	acg Thr	gtg Val	ctg Leu	1027
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ttgaaaa	atgʻ	cac												٠	1134
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												cac His		259
												ttg Leu		307
												tgt Cys		355
												cgc Arg 100		403
												atg Met		451
												gag Glu		499
												gtt Val		547
												tac Tyr		595
 		_	_	_	_			-	_	_	-	ggt Gly 180	-	643
	Val		Arg	Tyr	Asp	Asn	Leu			Gln		cgt Arg		691
												ggc Gly		739
												act Thr		787
												ccg Pro		835
												att Ile 260		883

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acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr 280 285 290	979
tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg 295 300 305	1027
agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp 310 315 320	1076
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Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr 50 . 55 60	
Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys 65 70 75 80	
Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val 85 90 95	
Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val	
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Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly 130 135 140	
Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly 145 150 155 160	
Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala 165 170 175	
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att to Ile So 70															355
tct g Ser V															403
atc ad Ile T		Arg													451
att to	rp I														499
gat c Asp L 1															547
ttc c Phe Lo 150															595
tca c Ser L	-		-		_			-		_		_		-	 643
gaa g Glu A		/al													691
gtg ge Val G	ly I														739
aaa co Lys P: 2			_			-	_		_			_			787
gag a Glu L 230				-			-			_	-	-		-	835
tac ta Tyr T															883
cat a		Ala													931
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35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp 245 . 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr 260 265 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu 275 280 285

Arg

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ctt aat ctq qca gac aac agc gag aga aag aag ccc atg ccg tca cca
                                                                   163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
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Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
             25
ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt
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Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
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                              45
cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att
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Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
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att too goo goa caa tog got gga acc tot too aat aag cag gto att
                                                                   355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70
                     75
                                                                   403
tot gto ato gtg gtt aaa gat oot gag otg agg aaa ggo oto gog ggg
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
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                 90
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg
                                                                   451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
            105
att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa
                                                                   499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
        120
                            125
gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg
                                                                   547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
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ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag
                                                                   595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
                                                             165
150
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gag aaa aac ctc gaa c Glu Lys Asn Leu Glu L 230 2				
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Pro Met Pro Ser Pro G 20 Ala Thr Trp Thr Pro P 35 Gln His Arg Ser Val A 50 Thr Ile Arg Thr Ile I	25 Pro Gln Trp Asn 40 Arg Arg Trp Leu 55	Ala Ala Arg Tyr Glu Thr Leu Asp 4: Asp Lys Pro Va.	15 r Gly Gln Pro 30 p Val Ile His 5	
Pro Met Pro Ser Pro G 20 Ala Thr Trp Thr Pro P 35 Gln His Arg Ser Val A 50 Thr Ile Arg Thr Ile I	Pro Gln Trp Asn 40 Arg Arg Trp Leu 55	Ala Ala Arg Ty: Glu Thr Leu Asg 4: Asp Lys Pro Va: 60 Gln Ser Ala Gly 75	15 r Gly Gln Pro 30 val Ile His Asp Asp Asp y Thr Ser Ser 80	
Pro Met Pro Ser Pro G 20 Ala Thr Trp Thr Pro P 35 Gln His Arg Ser Val A 50 Thr Ile Arg Thr Ile I 65 Asn Lys Gln Val Ile S	25 Pro Gln Trp Asn 40 Arg Arg Trp Leu 55 Ele Ser Ala Ala 70 Ser Val Ile Val	Ala Ala Arg Ty: Glu Thr Leu Asp 4! Asp Lys Pro Va: 60 Gln Ser Ala Gly 75 Val Lys Asp Pro 90	15 r Gly Gln Pro 30 P Val Ile His S l Asp Asp Asp y Thr Ser Ser 80 P Glu Leu Arg 95	
Pro Met Pro Ser Pro G 20 Ala Thr Trp Thr Pro P 35 Gln His Arg Ser Val A 50 Thr Ile Arg Thr Ile I 65 Asn Lys Gln Val Ile S 85 Lys Gly Leu Ala Gly I	25 Pro Gln Trp Asn 40 Arg Arg Trp Leu 55 Gle Ser Ala Ala 70 Ser Val Ile Val Gle Thr Arg Gln 105	Ala Ala Arg Ty: Glu Thr Leu Asp 4! Asp Lys Pro Va 60 Gln Ser Ala Gl 75 Val Lys Asp Pro 90 Met Phe Pro His	15 r Gly Gln Pro 30 P Val Ile His 5 l Asp Asp Asp y Thr Ser Ser 80 P Glu Leu Arg 95 S Leu Glu Gln 110 g Ile Ser Ala	
Pro Met Pro Ser Pro G 20 Ala Thr Trp Thr Pro P 35 Gln His Arg Ser Val A 50 Thr Ile Arg Thr Ile I 65 Asn Lys Gln Val Ile S 85 Lys Gly Leu Ala Gly I 100 Val Pro Ala Val Leu I	25 Pro Gln Trp Asn 40 Arg Arg Trp Leu 55 Ser Ala Ala 70 Ser Val Ile Val Ele Thr Arg Gln 105 Ele Trp Leu Ile 120	Ala Ala Arg Ty: Glu Thr Leu Asp 4! Asp Lys Pro Va: 60 Gln Ser Ala Gl: 75 Val Lys Asp Pro 90 Met Phe Pro His	To Gly Gln Pro 30 P Val Ile His 55 I Asp Asp Asp Asp You have a ser 80 P Glu Leu Arg 95 S Leu Glu Gln 110 G Ile Ser Ala 55	

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		gtg atc aag gac Val Ile Lys Asp 110		
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		gat acc ctc cac Asp Thr Leu His		
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		cca ctg ggt aag Pro Leu Gly Lys 190		
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Ile Leu Glu Leu 35	Leu Asp His	Val Asn Asn Lys 40	Phe Ile Glu Glu 45	Gly

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly 55 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu 170 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr 200 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala 230 235 Arg Ala Ala Phe Arg Gly Lys Asp Asp 245 <210> 713 <211> 929 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(906) <223> RXN03014 <400> 713 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr 10 ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met 20 25 gtq tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt

Val	Ser	Met 35	Ala	Ser	Ser	Met	Val 40	Phe	Leu	Phe	Gly	Leu 45	Ala	Met	Val	
	-		-		acg Thr	-		-	-		-			-	_	192
					gga Gly 70											240
	_				aaa Lys	-	_					_			_	288
-	-				acc Thr			-	-	-			-		_	336
					gtg Val											384
				-	gga Gly			-		-	-	_			-	432
	-		-		att Ile 150			-		-	-				-	480
		_	_	-	tca Ser			_	_	_					_	528
					ctt Leu											576
					cac His											624
					cgc Arg											672
					atc Ile 230											720
					ggt Gly											768
					gaa Glu											816
					agg Arg											864

275 280 285

cac cat ggt tct ggt ctg gtc caa ggc ctt ctg gcg cga ccg 906 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro 290 295 300

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<211> 302

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

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Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met 50 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gl
n Gly Leu Ser Gly Ala Ile 180 \$185\$ 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly

145	150	155	160
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3	cac att ctg gtt cag His Ile Leu Val Gln 200	_	
	cgc caa gcc gga tcc Arg Gln Ala Gly Ser 215		
	atc tcc cca ctt ctt Ile Ser Pro Leu Leu 230		
-	ggt ggt atc cca ccg Gly Gly Ile Pro Pro 250		
-	gaa gcc ggc gcc gaa Glu Ala Gly Ala Glu 265		-
	ggc gcc gtt gtc acc Gly Ala Val Val Thr 280		
	tgg tcc aag gcc ttc Trp Ser Lys Ala Phe 295		
	acc gca ctt gcg cga Thr Ala Leu Ala Arg 310		
	gcc gtt aaa gac cgc Ala Val Lys Asp Arg 330		
	ttc tcc act gct ctc Phe Ser Thr Ala Leu 345		
	gca gga cca ctg tca Ala Gly Pro Leu Ser 360		
	gat gtc aac atc tac Asp Val Asn Ile Tyr 375		
	cca tca cgc aca ctc Pro Ser Arg Thr Leu 390		

PCT/IB00/00943

WO 01/00844 245 250 255 Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly 265 Met Gly Pro Tyr Arg Arg Arg Cys His Leu Thr Ala His Leu Val 275 280 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro 295 <210> 715 <211> 1280 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1257) <223> FRXA00910 <400> 715 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc 48 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val 40 tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg 192 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc 240 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg 288 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca 336 Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala 100 105 ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg 384 Gly Leu Leu Thr Lys Val Gly Val Tyr Ser. Ile Ile Arg Ala Arg Ser 120 att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca 432 Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala 135 ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat 480 Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag 1248 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu 405 410 415

gac caa cca tgatcagtgg attcaaacga cga Asp Gln Pro 1280

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<212> PRT

<213> Corynebacterium glutamicum

<400> 716

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20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly 250 Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala 270 260 265 Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr 280 Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp 295 300 Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met 330 Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala 355 Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp Ala Asn Arq Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu 405 410 Asp Gln Pro <210> 717 <211> 1051 <212> DNA <213> Corynebacterium glutamicum <220> .<221> CDS <222> (101)..(1051) <223> RXN01895 <400> 717 cgcgtacacg tgctcaacac gacaacgctt aaacggctgc acgcgtaaca cggcagaccg 60 cacaagcttt aagatccacg atcaggagac tttgacaaat atg tca gtt aac cca 115 Met Ser Val Asn Pro 1 ace ege eee gaa gge egt eac eac gte gte gte ate ggt tet ggt 163 Thr Arg Pro Glu Gly Gly Arg His His Val Val Ile Gly Ser Gly 211 ttt ggt ggc ett ttt get gee aag aac etg gee aag gea gae gte gat Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp 25 35

				gac Asp												259
				acc Thr												307
				ctg Leu												355
gaa Glu	gtc Val	acc Thr	gac Asp	atc Ile 90	aac Asn	gtc Val	gag Glu	tcc Ser	cag Gln 95	act Thr	gtg Val	acc Thr	gcc Ala	tcc Ser 100	ctg Leu	403
				cgc Arg												451
				tcc Ser												499
				tcc Ser												547
				gag Glu												595
gaa Glu	cgc Arg	ctg Leu	ctc Leu	acc Thr 170	ttc Phe	gtc Val	gtt Val	gtt Val	ggc Gly 175	gct Ala	ggc Gly	cca Pro	acc Thr	ggt Gly 180	gtt Val	643
				cag Gln												691
	Tyr		Asn	ttc Phe	Asn	Thr	Asn	Ser	Ala		Ile	Ile	Leu			739
				gtt Val												787
				ctg Leu												835
				gtt Val 250												883
				acc Thr												931

gtt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt 979 Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val 285 280 gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt 1027 Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val 300 1051 ggc gat cag aag aac gtc ttc gtt Gly Asp Gln Lys Asn Val Phe Val 310 315 <210> 718 <211> 317 <212> PRT <213> Corynebacterium glutamicum <400> 718 Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser 105 Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His 120 Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu 135 Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu 150 155 Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His 185 Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys 215 220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr 245 Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val <210> 719 <211> 816 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(816) <223> FRXA01895 <400> 719 cac cac ctc ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu tee tee ggt gaa ate gea eet tee aet ega eag ate etg gge tee eag Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln qaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu 35 tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192 Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu 50 55 tac gat tee ttg gte gtt ggt get gge gea ggt eag tee tae tte gge 240 Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly 65 aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp 85 gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu 100 105 atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val 115

gtt ggc gct Val Gly Ala 130												432
atg gct cac Met Ala His 145	Arg Thr	_				-						480
tcc gca aag Ser Ala Lys				Ğİy								528
ttc ggt aag Phe Gly Lys	-		Asn A	-	-	_		_	-	-	_	576
ggt gtc aac Gly Val Asn 195	-	_	-	-	-			-	_	-		624
tcg gtc acc Ser Val Thr 210												672
ttc tgc aag Phe Cys Lys 225	Ile Trp											720
ctc gtc gca Leu Val Ala				Glu								768
atg gtt aac Met Val Asn			Val (816
<210> 720 <211> 272 <212> PRT <213> Coryne	ebacteriu	m glutan	nicum									
<400> 720 His His Leu	Phe Gln	Pro Leu	Len '	Tur	Gln	Val	Δla	Thr	Glv	Tle	ī.ėn	
1	5	IIO Dea	Dea .	- , -	10	, u			O1,	15	Dou	
Ser Ser Gly	Glu Ile 2	Ala Pro	Ser ?	Thr 25	Arg	Gln	Ile	Leu	Gly 30	Ser	Gln	
Glu Asn Val 35	Asn Val	Ile Lys	Gly (Glu	Val	Thr	Asp	Ile 45	Asn	Val	Glu	
Ser Gln Thr 50	Val Thr	Ala Ser 55	Leu (Gly	Glu	Phe	Thr 60	Arg	Val	Phe	Glu	
Tyr Asp Ser 65	Leu Val	Val Gly 70	Ala(Gly	Ala	Gly 75	Gln	Ser	Tyr	Phe	Gly 80	
Asn Asp His	Phe Ala (Glu Phe	Ala I	Pro	Gly 90	Met	Lys	Ser	Ile	Asp 95	Asp	

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu 105 100 Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val 120 Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu 135 140 Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn 150 155 Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro 170 165 Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val 250 Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val 265 260

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                                                                   115
                                            Met Thr Thr Pro Pro
act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg
                                                                   163
Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro
                                     15
gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg
                                                                   211
Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu
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25 30 35

					gct Ala											259
					ggc Gly											307
					aac Asn 75											355
gcc Ala	aag Lys	gcg Ala	gtc Val	gcc Ala 90	gag Glu	gaa Glu	aca Thr	aca Thr	cct Pro 95	gat Asp	cgt Arg	gcc Ala	ggc Gly	aaa Lys 100	gag Glu	403
					tct Ser											451
tgg Trp	ctg Leu	gga Gly 120	aag Lys	cgt Arg	ggc Gly	cga Arg	atc Ile 125	acc Thr	gag Glu	ccc Pro	atg Met	ttt Phe 130	tat Tyr	gat Asp	cgt Arg	499 [.]
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				-	aag Lys 155		-				•	-	-			595
					cga Arg											643
					ctt Leu											691
					acc Thr											739
					gtg Val											787
					aac Asn 235											835
-			-	_	aag Lys	-				_		_		_		883
					ggt Gly											931

					att Ile											979
					gac Asp											1027
					gcc Ala 315											1075
					acc Thr											1123
					tgc Cys											1171
					aag Lys											1219
					aag Lys											1267
		_	_		act Thr 395					_			_			1315
					cac His											1363
					ccg Pro											1411
			-		ccc Pro	_	_				-	-	_			1459
					gaa Glu											1507
					gtg Val 475											1555
					ctg Leu											1603
tca Ser	caa Gln	gca Ala	tgg Trp 505	cct Pro	ggt Gly	gag Glu	cag Gln	tca Ser 510	ctt Leu	atc Ile	ctt Leu	ccg Pro	gtg Val 515	att Ile	gct Ala	1651

	aca Thr															1699
	gat Asp 535															1747
	aag Lys															1795
	aag Lys															1843
	gat Asp															1891
gat Asp	ttc Phe	aac Asn 600	cgt Arg	cgc Arg	atc Ile	gac Asp	aac Asn 605	ccc Pro	ggt Gly	gga Gly	ttc Phe	ctc Leu 610	ctc Leu	ccc Pro	aac Asn	1939
	cct Pro 615															1987
	gtt Val								Leu							2035
	aac Asn															2083
	gat Asp															2131
	aat Asn					Lys		Arg			Lys					2179
	gat Asp 695															2227
	cga Arg															2275
	cct Pro															2323
	aac Asn															2371
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Gly Arg Thr Ala Ser 760

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<400> 722

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Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala 35 40 45

Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro 50 55 60

Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu 65 70 75 80

Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp 85 90 95

Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg 100 105 110

Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro 115 120 125

Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser 130 140

Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu 145 150 155 160

Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro 165 170 175

Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu 180 185 190

Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly 195 200 205

Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr 210 215 220

Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His 225 230 235 240

Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys 245 250 255

Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg 260 265 270

Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala 280 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln 300 295 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val Asn Phe Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly 410 Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe 440 Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile 505 Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val 520 Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr 535 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp 550 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln 570 Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr 580

Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly

600 595 605 Phe Leu Leu Pro Asn Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn 615 Gly Lys Ala Gln Leu Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro 630 635 Lys Asp Tyr Leu Leu Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn 650 Ser Thr Ile Tyr Gly Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly 660 665 Arg Arg Val Val Phe Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu Arg Arg Ala Pro Asn Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp 725 Ser Val Ala Glu Lys Ser Asn Thr Pro Val Ser Lys Ser Val Val Val 745 Arg Leu Glu Ala Thr Gly Arg Thr Ala Ser <210> 723 <211> 1038 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1015) <223> RXN00705 <400> 723 gttctggaac aagcactgat gattgggccg agtccacgtt ggttaatgct ctgcatcttc 60 aagaaatcat cgctaaaaat tacccggagg ctaaataaaa atg ggt cgg att acc 115 Met Gly Arg Ile Thr 1 caa aac ttg cag gtc cca cgc gtt gtg tcc act gac gag caa gtt ttt 163 Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe 15 10 gtt aac act cgt ccg gat act gtt gcg gtg gag gag cct cta gaa att 211 Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile 25 30 egg gtt aat gge act geg ett ace ace act atg ege acg eee gge eat

Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His

45

40

gat Asp	att Ile 55	gag Glu	ttg Leu	gtg Val	cat His	ggc Gly 60	ctc Leu	ctc Leu	ttg Leu	tca Ser	gaa Glu 65	ggt Gly	ctg Leu	atc Ile	acg Thr	307
		tct Ser														355
		aat Asn														403
		aat Asn														451
_		agc Ser 120			_	_								_	•	499
		cta Leu														547
-	_	ggt Gly	-	-		_	_			-	_	_	_		-	595
		tgg Trp														643
		cca Pro														691
		gtt Val 200														739
		cga Arg		_	_					_	-	_		_		787
		atg Met														835
		agt Ser														883
		att Ile														931
		gcg Ala 280														979

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Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Met 35 40 45

Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser 50 60

Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys
65 70 75 80

Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu 85 90 95

Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn 100 105 110

Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro 115 120 125

Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn 130 135 140

Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu 145 150 155 160

Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp 165 170 175

Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys 180 185 190

Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu 195 200 205

Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala 210 215 220

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu 225 230 235 240

Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val 245 250 255

Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu 280 275 Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu 295 Gly 305 <210> 725 <211> 908 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(885) <223> FRXA00705 <400> 725 cca cqc qtt qtq tcc act gac gag caa gtt ttt gtt aac act cgt ccg 48 Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro-5 gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr . 20 gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144 Ala Leu Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val 35 cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192 His Gly Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val 50 240 ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala 85 90 336 egg gat eee gte eag aat eee tee eat aat eee gaa gge age eaa eae Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His 110 100 105 gaa qea ete cae ate eea aet tte caa eeg gta ege gaa eta aac ete 384 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu 115 120 125 gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys 130 135 140 480 ggc acg acg tct att gag cag ttg atg aac aag aag ggc tgg ccc att

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gct ggt ttg Ala Gly Leu 195	gcc acg Ala Thr	ctt Leu	gat Asp	ggt Gly 200	gag Glu	atg Met	ttg Leu	att Ile	att Ile 205	cga Arg	gag Glu	gat Asp	624
gtc ggt cgg Val Gly Arg 210													672
gcg gga aag Ala Gly Lys 225													720
gcg tct ttt Ala Ser Phe		Val											768
gta atc gct Val Ile Ala													816
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Arg	Asp	Pro	Val 100	Gln	Asn	Pro	Ser	His 105	Asn	Pro	Glu	Gly	Ser 110	Gln	His	
Glu	Ala	Leu 115	His	Ile	Pro	Thr	Phe 120	Gln	Pro	Val	Arg	Glu 125	Leu	Asn	Leu	
Val	Ala 130	Ala	Gln	Arg	Asn	Val 135	Leu	Thr	Thr	Ser	Ala 140	Cys	Gly	Val	Cys	
Gly 145	Thr	Thr	Ser	Ile	Glu 150	Gln	Leu	Met	Asn	Lys 155	Lys	Gly	Trp	Pro	Ile 160	
Thr	Pro	Ile	Thr	Pro 165	Asp	Pro	Arg	Met	Ile 170	Val	Ser	Leu	Pro	Asp 175	Lys	
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Ala	Gly	Leu 195	Ala	Thr	Leu	Asp	Gly 200	Glu	Met	Leu	Ile	Ile 205	Arg	Glu	Asp	
Val	Gly 210	Arg	His	Asn	Ala	Ala 215	Asp	Lys	Val	Ile	Gly 220	Asn	Met	Leu	Met	
Ala 225	Gly	Lys	Leu	Pro	Leu 230	Glu	Asn	Thr	Ile	Leu 235	Val	Met	Ser	Ser	Arg 240	
Ala	Ser	Phe	Glu	Leu 245	Val	Gln	Lys	Ala	Ala 250	Met	Ala	Gly	Ile	Ser 255	Gly ·	
Val	Ile	Ala	Val 260	Gly	Ala	Ala	Thr	Ser 265	Leu	Ala	Ile	Glu	Ala 270	Ala	Gln	
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caa	acg	tat	qcg	cag	ttc	tca	gac	act	gcc	ttc	gta	tcg	gca	tac	atc	163

Gln Thr Tyr	Ala Gln 10		r Asp	Thr	Ala 15	Phe	Val	Ser	Ala	Tyr 20	Ile	
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gtt ggt gca Val Gly Ala 55		Ser Al										307
atc gcc gad Ile Ala Asp 70												355
acc gca cgo Thr Ala Aro		Ala As										403
gtc atg gto Val Met Val												451
cga ttc ccc Arg Phe Pro 120	Phe Gly											499
ttc gcc ato Phe Ala Met 135			l Leu									547
gtg gta tgg Val Val Trg 150												595
ggt ggc acc Gly Gly Thi		Tyr Se										643
cag tcc ttc Gln Ser Phe		-		_			-				-	691
tcc atc ggt Ser Ile Gly 200	Ile Val											739
ata taa aa			a maa	aaq	ggc	ttc						787
Met Trp Glr 215	cca aag Pro Lys		s Glu			Phe	Phe 225	Gly	Ala	Val	Ala	
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250 255 260 atc tgg gca gaa gcc tgg ggt cgt ttc tgg gga tgg gat cct aag Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys 270 gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His 280 285 gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac 1027 Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn 295 300 atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg 1075 Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met 320 310 315 gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt 1121 Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn 330 335 1134 tggttggcgg ggt <210> 728 <211> 337 <212> PRT <213> Corynebacterium glutamicum <400> 728 Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile 120 Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln 130 Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu 150 155

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Val	Val	Pro	Ala 180	Leu	Gln	Ser	Phe	Trp 185	Phe	Pro	Ile	His	Val 190	Ser	Ser	
Val	Ser	Ile 195	Gly	Ala	Ser	Ile	Gly 200	Ile	Val	Ser	Gly	Ile 205	Ala	Ser	Leu	
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Phe 225	Gly	Ala	Val	Ala	Lys 230	Pro	Leu	Pro	Ser	Gly 235	Lys	Thr	Leu	Asp	Asn 240	
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Ile	Ile	Leu	Gly 260	Ala	Ile	Trp	Ala	Glu 265	Ala	Ala	Trp	Gly	Arg 270	Phe	Trp	
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									atc Ile							96
									gaa Glu							144
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Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp 55 240 ege aac ace aac get gea tgg ate aac ate etg geg etg gte aeg atg Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met 75 70 att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct 288 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser 85 90 326 tac gcc gga ctg aac taagcacttt tggttggcgg ggt Tyr Ala Gly Leu Asn 100 <210> 730 <211> 101 <212> PRT <213> Corynebacterium glutamicum <400> 730 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser 90 85 Tyr Ala Gly Leu Asn 100 <210> 731 <211> 610 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(610) <223> FRXA00386 <400> 731 gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60 acatcgaage agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac Met Leu Pro Val Asn 1

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atc tac gtt ctg Ile Tyr Val Leu 25	Ala Leu Il	c ctc tcc ct e Leu Ser Le 30	cc gtc tac tac eu Val Tyr Tyr	gta aaa caa 211 Val Lys Gln 35
caa ggc att atc Gln Gly Ile Ile 40				
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atc gcc gac ggt Ile Ala Asp Gly 70				
acc gca cgc aaa Thr Ala Arg Lys		n Met Thr G		
gtc atg gtg cac Val Met Val His 105	Leu Val Se			
cga ttc ccc ttc Arg Phe Pro Phe 120				
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Arg Val Ser Glu	ı Leu Val Gl	y Ala Gly G	ly Ser Ala Asp	Val Asp Thr

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Ala	Lys	Arg	Glu	Glu 85	Thr	Ala	Arg	Lys	Leu 90	Ala	Asn	Met	Thr	Gln 95	Ser	
Leu	Met	Trp	Leu 100	Gly	Val	Met	Val	His 105	Leu	Val	Ser	Val	Val 110	Met	Arg	
Ala	Leu	Ser 115	Ala	Ser	Arg	Phe	Pro 120	Phe	Gly	Asn	Leu	Tyr 125	Glu	Tyr	Ile	
Leu	Met 130	Val	Thr	Leu	Phe	Ala 135	Met	Ile	Gly	Ala	Val 140	Leu	Ile	Leu	Gln	
Arg 145	Pro	Gln	Phe	Arg	Val 150	Val	Trp	Pro	Trp	Ile 155	Leu	Thr	Pro	Met	Ala 160	
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					at to						atg		gaa	cgc	ctc	115
aaa Lys	cgc Arg	cta Leu	gat Asp	ccg Pro 10	ctc Leu	att Ile	gtc Val	ctc Leu	att Ile 15	gtg Val	ctg Leu	gct Ala	gtc Val	att Ile 20	gtg Val	163
					gtt Val											211
					att Ile											259
					gcg Ala											307
					atc Ile 75											355

ggg ctc gag Gly Leu Glu											403
att ttg ttc Ile Leu Phe											451
ttt acc tcg Phe Thr Ser 120											499
tcg ctc tcc Ser Leu Ser 135	aac ctt q Asn Leu A	gcg ggt Ala Gly 140	gtt ttc Val Phe	ctc Leu	act Thr	ccg Pro 145	ctg Leu	ctg Leu	gtc Val	atg Met	547
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ctc gac att Leu Asp Ile											643
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gtg gac cgc Val Asp Arg 200	ggc tcg a	atc gcg Ile Ala	atg gtc Met Val 205	gtg Val	tac Tyr	tcc Ser	gcg Ala 210	ttt Phe	tct Ser	gcc Ala	739
ggc atg gtg Gly Met Val 215	gct ggc a	att tgg Ile Trp 220	tcc act Ser Thr	gtg Val	agc Ser	gtt Val 225	cta Leu	gag Glu	att Ile	atc Ile	787
tac ctc att Tyr Leu Ile 230	Val Phe										835
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gct att cag Ala Ile Gln				Ser							931
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ccg ttg atg Pro Leu Met 295											1027
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Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys 50 55 60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe 65 70 75 80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu 85 90 95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val 100 105 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
115 120 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr 130 135 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Val His Val 145 150 155 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe 165 170 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn 180 185 190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr 195 200 205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser 210 220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met 225 230 235 240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn 245 250 255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu 260 265 270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile 275 280 285

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Val	Ala 135	Glu	Ala	Trp	Asp	Ala 140	Val	Tyr	Trp	Ile	Met 145	Ala	Asn	Val	Leu	
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-	_		cgc Arg	-	-					_	_	-		-	-	643
			gaa Glu 185													691
			acc Thr													739
_	-	-	tac Tyr	_	_									_		787
			gat Asp													835
			gac Asp													883
		-	gac Asp 265				-		-			_				931
			atg Met			-		-		-			_	_	_	979
_		-	ttg Leu		-	-	_	-						_		1027
			cag Gln													1075
			cgc Arg													1123
			gcg Ala 345				_	-				_		_	_	1171
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35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp 195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala 245 250 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met 280 275 Asn Pro Glu Arg Asp Val Val Leu His Ala Asp Gln Ala Glu Ser 295 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro 315 310 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly 340 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arq Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser 385 <210> 737 <211> 1281 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1258) <223> FRXA02556 <400> 737 tqccatcata ttaaqqccaa attqcttqqa tcctqqqatt tatttaatta gattaaatcc 60 gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc Leu Ile Val Ser Thr cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val 10 15 211 ate aaa gea aeg ett eet ete gtg gge gge aag att aat gag ate aeg Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr 30 259 ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala 45 307 aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala ctq gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp

70					75					80					85	
-		-		-	-	-	-		cgc Arg 95				_			403
					-	-	-		gac Asp		_				-	451
	-	_		-		_	_		gcg Ala	-		-		_		499
									tgg Trp							547
								-	tcc Ser		-	_				595
-	_		-	-	-		-		gcg Ala 175	_	-	_		_	_	643
	_		_			_	-		gag Glu	-	-	-				691
									ctt Leu							739
_	-	_		_	_				tcc Ser	_				-		787
	•		-				-		gga Gly		_	-	-	-	-	835
									atc Ile 255							883
									ctg Leu							931
									ggt Gly							979
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								tgg Trp								1123
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	_	_		-				ctc Leu	_		-		_	-	-	1219
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Glu	His	Ala	Glu 20	Val	Ile	Lys	Ala	Thr 25	Leu	Pro	Leu	Val	Gly 30	Gly	Lys	
Ile	Asn	Glu 35	Ile	Thr	Pro	Val	Phe 40	Tyr	Asn	Lys	Met	Phe 45	Ala	Ala	His	
Pro	Glu 50	Leu	Ile	Ala	Asn	Thr 55	Phe	Asn	Gly	Gly	Asn 60	Gln	Lys	Gln	Gly	
Asp 65	Gln	Gln	Lys	Ala	Leu 70	Ala	Ala	Ser	Ile	Ala 75	Thr	Phe	Ala	Thr	Met 80	
Leu	Val	Thr	Pro	Asp 85	Ala	Pro	Asp	Pro	Val 90	Gln	Leu	Leu	Ser	Arg 95	Ile	
Gly	His	Lys	His 100	Val	Ser	Leu	Gly	Ile 105	Thr	Ala	Asp	Gln	Tyr 110	Asp	Ile	
Val	His	Glu 115	His	Leu	Phe	Ala	Ala 120	Ile	Val	Glu	Val	Leu 125	Gly	Ala	Glu	
Thr	Val 130	Thr	Ala	Pro	Val	Ala 135	Glu	Ala	Trp	Asp	Ala 140	Val	Tyr	Trp	Ile	
Met 145	Ala	Asn	Val	Leu	Ile 150	Gly	Phe	Glu	Asn	Asn 155	Leu	Tyr	Ala	Ser	Asn 160	
Asp	Leu	Glu	Pro	Gly 165	Asp	Val	Phe	Arg	Glu 170	Val	Thr	Val	Thr	Ala 175	Lys	
Lys	Gln	Leu	Ser 180	Ala	Thr	Val	Trp	Glu 185	Tyr	Thr	Leu	Ala	Gly 190	Glu	Leu	

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe 235 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala 250 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile 260 265 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met 280 Asn Pro Glu Arg Asp Val Val Leu His Ala Asp Gln Ala Glu Ser 295 300 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro 310 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu 375 380 Ile Ser 385 <210> 739 <211> 1200 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1177) <223> RXA01392 <400> 739 qtctqcaatc accccqaaca tttqttcaat cqttqatttt cattccactt cqtaatattq 60 ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca Val Ala Asn Thr Ser tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe

		gat Asp														211
		tcc Ser 40														259
		gct Ala														307
		cgc Arg														355
atc Ile	tcg Ser	ctt Leu	ggt Gly	ctg Leu 90	acc Thr	ggc Gly	ccg Pro	act Thr	cac His 95	gac Asp	gtt Val	cgt Arg	tcc Ser	tgg Trp 100	act Thr	403
		tta Leu														451
		gac Asp 120														499
		cca Pro														547
_		cct Pro					-						_	_		595
		gag Glu														643
		ccg Pro	Val	Met	Lys	Arg	Ile	Phe		Glu	Val		Asn	Gly		691
		acc Thr 200														739
		ctt Leu														787
cga Arg 230	cgt Arg	tac Tyr	ctc Leu	atg Met	ggg Gly 235	gat Asp	cac His	atc Ile	acc Thr	gag Glu 240	gcg Ala	gat Asp	atc Ile	cgc Arg	ctc Leu 245	835
		acc Thr														883

-		-		-			-	_	-			 ggc Gly 275	-	931
							-					gat Asp		979
-		-	-									aac Asn		1027
		-		-			_	_				 aca Thr		1075
	_	-	_							-	_	 gtt Val	_	1123
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Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly
35 40 45

Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala 50 55 60

Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu 65 70 75 80

Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp 85 90 95

Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val 100 105 110

Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp 115 120 125

Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys 130 135 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu 155 145 150 Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala 170 Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu 185 180 Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu 215 210 Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn 265 Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp 275 280 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala 295 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Val Lys Asn Pro Glu Pro Phe Gln Lys 355 <210> 741 <211> 1227 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1204) <223> RXA00800 <400> 741 gactccgcag ggatggccta caagtacggt cacggactta atttctagat tgtaggtagt 60 ctcgtgggca caactgaaat cttattgaaa aggagtgtcc atg agc act gta gtg Met Ser Thr Val Val 1

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gtt Val	gtt Val	gtc Val	cct Pro 25	gat Asp	cca Pro	ggt Gly	gct Ala	aac Asn 30	gat Asp	gtc Val	atc Ile	gtc Val	aag Lys 35	att Ile	cag Gln	211
gcc Ala	tgc Cys	ggt Gly 40	gtg Val	tgc Cys	cac His	acc Thr	gac Asp 45	ttg Leu	gcc Ala	tac Tyr	cgc Arg	gat Asp 50	ggc Gly	gat Asp	att Ile	259
tca Ser	gat Asp 55	gag Glu	ttc Phe	cct Pro	tac Tyr	ctc Leu 60	ctc Leu	ggc Gly	cac His	gag Glu	gca Ala 65	gca Ala	ggç Gly	att Ile	gtt Val	307
gag Glu 70	gag Glu	gta Val	ggc Gly	gag Glu	tcc Ser 75	gtc Val	acc Thr	cac His	gtt Val	gag Glu 80	gtc Val	ggc Gly	gat Asp	ttc Phe	gtc Val 85	355
atc Ile	ttg Leu	aac Asn	tgg Trp	cgt Arg 90	gca Ala	gtg Val	tgc Cys	ggc Gly	gag Glu 95	tgc Cys	cgt Arg	gca Ala	tgt Cys	aag Lys 100	aag Lys	403
ggc Gly	gag Glu	cca Pro	aag Lys 105	tac Tyr	tgc Cys	ttt Phe	aac Asn	acc Thr 110	cac His	aac Asn	gcc Ala	tct Ser	aag Lys 115	aag Lys	atg Met	451
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								gaa Glu								547
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								acc Thr								643
								ggc Gly 190								691
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								ggt Gly								835
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Lys var Arg Gi	Leu Thr 250	Asp Gly	Phe Gly 255	Thr Asp	Val		Ile 260	Asp	
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cat gca ggc cg His Ala Gly Arc 280	: atg gtg Met Val	atg gtg Met Val 285	Gly Val	cca aac Pro Asn	ctg Leu 290	acg f	tct Ser	cgc Arg	979
gta gat gtt cc Val Asp Val Pro 295									1027
cct gca tgg ta Pro Ala Trp Ty: 310		Cys Leu							1075
gtg gat ctg ca Val Asp Leu Hi	ctg cag Leu Gln 330	ggt cgt Gly Arg	ttc cca Phe Pro 335	ctg gat Leu Asp	aag Lys	Phe '	gtt Val 340	tct Ser	1123
gag cgt att gg Glu Arg Ile Gl 34	Leu Asp	gat gtt Asp Val	gaa gag Glu Glu 350	gct ttc Ala Phe	Asn	acc a Thr I 355	atg Met	aag Lys	1171
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gcg									1227
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Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala 115 120 125

Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln 130 135 140

Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu 145 150 155 160

Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp 165 170 175

Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly 180 185 190

Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile 195 200 205

Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly 210 215 220

Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala 225 230 235 240

Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr 245 250 255

Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala 260 265 270

Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro 275 280 285

Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg 290 295 300

Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg 305 310 315 320

Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu 325 330 335

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Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met Leu Thr Gly Pro Gln 220 aac atg cct aag ttc tcc gat cgt cag ctc tcc gca gat gag aag aag 835 Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser Ala Asp Glu Lys Lys 235 240 gac atc atc gcc ttc atc aag tcc acc aag gag act cca tca cct ggt 883 Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu Thr Pro Ser Pro Gly 250 255 931 ggt tac tca ctc ggt agc ttg ggc cca gtg gct gag ggt ctg ttc atg Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met 270 979 tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala Ala Met Trp Ile Gly tca cgt tca tgagtaacaa caacgacaaa cag 1011 Ser Arg Ser 295 <210> 744 <211> 296 <212> PRT <213> Corynebacterium glutamicum <400> 744 Met Met Glu Thr Asn Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys Pro Ser Ala Lys Lys Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser 105 Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala 115 120 Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala 135 Ala Asn Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu 160 145 150 155 Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser